JC16 Rec'd PCT/PTO SEP 1 7 2001

FORM-PTO-1390 (Rev. 12-29-99) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY'S DOCKET NUMBER 012627-025
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371		U.S. APPLICATION NO. (If known, see 37 C.F.R. 1.5) UNASSIGNED 09/936738
INTERNATIONAL APPLICATION NO. PCT/EP00/02330	INTERNATIONAL FILING DATE 21 SEPTEMBER 2000	PRIORITY DATE CLAIMED 19 MARCH 1999 31 DECEMBER 1999

TITLE OF INVENTION
Method for Identifying Organisms by Means of Comparative Genetic Analysis and Primers and Hybridization Probes for Carrying out this Method

APPLICANT(S) FOR DO/EO/US
Hans SCHACKERT et al.

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☐ This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and the PCT Articles 22 and 39(1).
4. ☐ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
   a. ☒ is transmitted herewith (required only if not transmitted by the International Bureau).
   b. ☐ has been transmitted by the International Bureau.
   c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
   a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
   b. ☐ have been transmitted by the International Bureau.
   c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
   d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☐ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern other document(s) or information included:

11. ☒ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A FIRST preliminary amendment.
    ☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information:

International Search Report
International Preliminary Examination Report
PCT Request form (PCT/RO/101)
(8) sheets of Drawings
(48) Sheets (List of species sequences)

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U.S. APPLICATION NO (If known, see 37 CFR 1.5) UNASSIGNED 09/936738	INTERNATIONAL APPLICATION NO. PCT/EP00/02330	ATTORNEY'S DOCKET NUMBER 012627-025

17. ☐ The following fees are submitted:	CALCULATIONS	PTO USE ONLY
Basic National Fee (37 CFR 1.492(a)(1)-(5)): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO .... $1,000.00 (960) International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO .... $860.00 (970) International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO .... $710.00 (958) International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4) .... $690.00 (956) International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4) $100.00 (962)		
ENTER APPROPRIATE BASIC FEE AMOUNT =	$ 860.00	
Surcharge of **$130.00 (154)** for furnishing the oath or declaration later than 20 ☐ 30 ☐ months from the earliest claimed priority date (37 CFR 1.492(e)).	$	

Claims	Number Filed	Number Extra	Rate		
Total Claims	52 -20 =	32	X$18.00 (966)	$ 576.00	
Independent Claims	21 -3 =	18	X$80.00 (964)	$ 1440.00	
Multiple dependent claim(s) (if applicable)			+ $270.00 (968)	$	
TOTAL OF ABOVE CALCULATIONS =				$ 2016.00	
Reduction for 1/2 for filing by small entity, if applicable (see below).				$	-
SUBTOTAL =				$ 2876.00	
Processing fee of **$130.00 (156)** for furnishing the English translation later than 20 ☐ 30 ☐ months from the earliest claimed priority date (37 CFR 1.492(f)). +				$	
TOTAL NATIONAL FEE =				$ 2876.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). **$40.00 (581)** per property +				$	
TOTAL FEES ENCLOSED =				$ 2876.00	
				Amount to be: refunded	$ -
				charged	$

a. ☐ Small entity status is hereby claimed.

b. ☒ A check in the amount of $ 2876.00 to cover the above fees is enclosed.

c. ☐ Please charge my Deposit Account No. 02-4800 in the amount of $______ to cover the above fees. A duplicate copy of this sheet is enclosed.

d. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 02-4800. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

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30,427
REGISTRATION NUMBER

Patent
Attorney's Docket No. 012627-025

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of

Prof. Dr. Hans SCHACKERT et al.

Application No.: Unassigned
(Corresponding to PCT/EP00/02330

International Filing Date: 16 March 2000

For: METHOD FOR IDENTIFYING ORGANISMS BY MEANS OF COMPARATIVE GENETIC ANALYSIS AND PRIMERS AND HYBRIDISATION PROBES FOR CARRYING OUT THIS METHOD

Group Art Unit: Unassigned

Examiner: Unassigned

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Prior to examination, kindly amend the above-identified application as follows:

IN THE CLAIMS:

Kindly replace claims 1-45 and 47-52 as follows:

1. (Amended) A method of identifying organisms by comparative genetic analysis, wherein the coding and/or non-coding areas and/or functionally significant areas of highly conserved genes and/or their homologous genes and/or their cDNA copies and/or their pseudogenes are amplified using PCR and are subsequently genotyped and analyzed.

2. (Amended) The method according to claim 1, wherein one primer pair each is used for each specific segment of the highly conserved gene, which is located in the highly conserved exon region and/or non-coding areas and/or functionally significant areas and/or in the 5'- or 3'-untranslated area of the gene and binds in as many studied species DNAs as possible, preferable in all studied species DNAs, and enables the amplification of the corresponding gene area.

3. (Amended) The method according to claim 1, wherein the coding and/or non-coding areas located between the primers and being either highly variant intron regions and/or variant exon regions or 5'- or 3'-untranslated areas of the gene, are analyzed as regards their sequence and identified by comparison with the species-specific sequence variants.

4. (Amended) The method according to claim 1, wherein either the sense strand or the antisense strand of any species DNA or also their PCR copies are used for the identification.

5. (Amended) The method according to claim 1, wherein animals are identified.

6. (Amended) The method according to claim 1, wherein vertebrates are identified.

7. (Amended) The method according to claim 1, wherein mammals are identified.

8. (Amended) The method according to claim 1, wherein plants are identified.

9. (Amended) The method according to claim 1, wherein genotying is carried out by DNA sequencing, any hybridization method, restriction fragment length analyses, chromatographic methods, spectroscopic and mass-spectroscopic methods, allele-specific PCR or by other methods suitable for detecting DNA sequence variants.

10. (Amended) The method according to claim 1, wherein exon and/or intron areas as well as functionally significant areas of the highly conserved tumor suppressor gene PTEN/MMAC1 and its homologues are used for amplification and subsequent genetic analysis.

11. (Amended) The method according to claim 1, wherein cDNA copies of the PTEN/MMAC1 gene and its homologues are used for the genetic analysis.

12. (Amended) The method according to claim 1, wherein pseudogenes or segments of pseudogenes of the PTEN/MMAC1 gene and its homologues are used for the genetic analysis.

13. (Amended) The method according to claim 1, wherein exons arranged next to the PTEN/MMAC1 gene and its homologues and/or the parts of the introns following the exons are analyzed genetically.

14. (Amended) The method according to claim 1, wherein the exon regions 1 and 2 and/or 3 and 4 and/or 4 and 5 and/or 5 and 6 and/or 6 and 7 and/or 7 and 8 and/or 8 and 9 with the enclosed intron regions 1 and/or 2 and/or 3 and/or 4 and/or 5 and/or 6 and/or 7 and/or 8 as well as the 5'- and 3'-untranslated regions of the PTEN/MMAC1 gene and their homologues are used for the genetic analysis.

15. (Amended) The method according to claim 1, comprising selecting areas of highly conserved genes and/or pseudogenes and their homologues, constructing suitable oligonucleotides as primers which bind to the corresponding complementary coding and/or non-coding areas and/or functionally significant areas, amplifying them by means of a suitable technique and comparatively analyzing the sequence of the corresponding coding and/or non-coding area of various species by genetic analysis.

16. (Amended) The method according to claim 15, wherein areas of the PTEN/MMAC1 gene and/or the pseudogene and their homologues are selected.

17. (Amended) The method according to claim 15, wherein differing sequence segments of each individual exon, intron or untranslated region of the PTEN/MMAC1 gene and their homologues or the corresponding cDNA are selected.

18. (Amended) The method according to claim 1, wherein genotyping of pig DNA which is obtained from foodstuffs, is carried out on the basis of the gene sequence variant of PTEN/MMAC1 containing a 9-base pair long deletion.

19. (Amended) An oligonucleotide primer for the PCR and the sequencing of exon 1 and/or 5'-untranslated region of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex1-401 sense

5'-cccttctactgcctcca -3'

PTENex1 -465 sense

5'- gggaggggggtctgagt -3'

PTENex1 ATG sense

5'- atgacagccatcatcaaaga -3'

PTENex1 R antisense

5'- aggtcaagtctaagtcgaatc -3'

20. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 2 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex2F sense

5'- atatttatccaaacattattgctat -3'

PTENex2R antisense

5'- cttactacatcatcaatattgttcc -3'

21. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 4, intron 4 and exon 5 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

Zoo43sUV sense

5'- tgtgctgagagacattatgac -3'

SPL5 sense

5'- aaatttaattgcagaggt -3'

Zoo44aRV antisense

5'- ttgtctctggtccttacttc -3'

22. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 5 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTEN se sense

5'- atcttgaccaatggctaagtg -3'

Zoo44aRV antisense

5'- ttgtctctggtccttacttc -3'

23. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 6 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex6F sense

5'- gga gta act att ccc agt cag ag -3'

PTENex6R antisense

5'- gca agt tcc gcc act gaa -3'

24. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 7 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex7F sense

5'- cct cag ttt gtg gtc tgc ca -3'

PTENex7R antisense

5'- c ctt ttt tag cat ctt gtt ctg ttt -3'

25. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 8 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex8F sense

5'- caa aat gtt tca ctt ttg ggt aaa -3'

PTENex8R antisense

5'- taa aat ttg gag aaa agt atc ggt t -3'

26. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 9 of the PTEN/MMAC1 gene and its homologues, comprising the following sequences:

PTENex9F sense

5'- gtg aag ctg tac ttc aca aaa ac -3'

PTENex9tga antisense

5'- aaa aaa att cag act ttt gta att tg -3'

27. (Amended) The method according to claim 1, wherein the DNA amplification involves a mixture of oligonucleotides which differ at the 3' region of the oligonucleotide as regards its length by one or more nucleotides or which differ as regards their nucleotide sequence at the 3' end of the oligonucleotide at one or more positions.

28. (Amended) The method according to claim 1, wherein the oligonucleotides

sense:

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat t -3',

antisense:

5' - cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc t -3'

are used for the amplification.

29. (Amended) The method according to claim 1, wherein the oligonucleotides

sense:

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gaa -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gag -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gat -3',

antisense:

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt a -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt g -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt t -3'

are used for the amplification.

30. (Amended) The method according to claim 1, wherein DNA sequencing methods are used for the genetic analysis.

31. (Amended) The method according to claim 1, wherein DNA sequencing techniques are used in the genetic analysis for the PTEN/MMAC1 and/or its pseudogenes and their homologues.

32. (Amended) The method of distinguishing the DNA of various species, wherein at least one hybridization probe pair is used, the melting points of different combinations are determined and compiled for each species into a panel.

33. (Amended) The method of distinguishing the DNA of various species, wherein at least one hybridization probe pair is used and at least one gene segment is amplified, differing hybridization probe pairs hybridize to different gene segments, and the melting points of the different combinations are determined and compiled for each species into a panel and/or compared with this panel for the purpose of identification.

34. (Amended) The method of distinguishing the DNA of different species according to claim 33, wherein at least one hybridization probe pair is used and at least one gene segment of at least one species is amplified, differing hybridization probe pairs hybridize to different gene segments of various species, and the melting points of the different combinations are determined and compiled for each species into a panel and/or compared with this panel for the purpose of identification.

35. (Amended) The method of distinguishing the DNA of various species according to claim 33, wherein at least two hybridization probes of SEQ Nos. 3 to 8 are used, the melting points of different combinations are determined and compiled for each species into a panel.

36. (Amended) The method according to claim 33, wherein the species differentiation of pig DNA from various other species is made using the hybridization probe pair Al/A2 as the hybridization probe pair.

37. (Amended) The method according to claim 33, wherein the hybridization probes are used in combinations Cl/C2; A1/B2; A1/A2; C1/A2; B1/B2; B1/A2 for the species differentiation between various species.

38. (Amended) LightCycler hybridization probes for exon 5, comprising the sequences:

A1: 5'- tgc ata ttt gtt tca tcc ggg caa att -fluorescein -3'

A2: 5'- LC Red 705 - tta aag gca caa gat ttc tat ggg ga - ph -3'

B1: 5'- tgc ata ttt att aca tcg ggg caa att -fluorescein -3'

B2: 5'- LC Red 640 - aag gca caa gag gcc cta gat ttc ta - ph -3'

C1: 5'-tgc ata ttt gtt aca tcg ggg taa att fluorescein -3'

C2: 5'- LC Red 640 - aag gca caa gag gcc cta gat ttc ta - ph -3'

39. (Amended) LightCycler hybridization probes for exon 6, comprising the sequences

PTENex6FL

5'- tca tct gga tta tag acc agt ggc act - fluorescein -3'

PTENex6LC 640

5'- LC Red 640 - ttc aca aga tga tgt ttg aaa cta ttc caa- ph -3'

PTENex6F*

5'- gtg cca ctg gtc tat aat cca gat- fluorescein -3'

PTENex6L* 705

5'- LC Red 705- ttc ttt aac agg tag cta taa taa tac aca ta- ph -3'

40. (Amended) LightCycler hybridization probes for exon 7, comprising the sequences

PTENex7F*

5'- taa agg tga aga tat att cct cca att ca - fluorescein -3'

PTENex7L*640

5'-LC Red 640- acc cac acg acg gga aga caa g - ph -3'

PTENex7 FL

5'-ggtaacggctgagggaactcaaagtac - fluorescein -3'

PTENex7 LC (705-labeled)

5'-LC Red 705- tgaacttgtcttcccgtcgtgtgg- ph -3'

41. (Amended) LightCycler hybridization probes for exon 8, comprising the following sequences

PTENex8F*

5'- tga caa gga ata tct agt act tac ttt aac aaa-fluorescein -3'

PPTENex8L* 705

5'-LC Red 705 - ctt gac aaa gca aat aaa gac aaa gc- ph -3'

PTENex8 FLU

5' - tgctatcgatttcttgatcacatagacttccatttt - fluorescein -3'

PTENex8 LCR (640-labeled)

5'-LC Red 640- actttttctgaggtttcctctggtcctggtat - ph -3'

42. (Amended) [The] LightCycler hybridization probes for exon 9, comprising the following sequences

PTENex9 FL

5'-aac atc tgg tgt tac aga agt tga act gct- fluorescein -3'

PTENex9 LC 640

5'-LC-640- cct ctg gat ttg acg gct cct cta ct - ph -3'

43. (Amended) Hybridization probe pair AI/A2: specific to PTEN pseudogene pig, comprising

SEQ No. 3 A1: 5'- tgc ata ttt gtt tca tcc ggg caa att -fluorescein -3'

SEQ No. 4 A2: 5'-LC Red 705- tta aag gca caa gat ttc tat ggg ga - ph -3'

44. (Amended) Hybridization probe pair B1/B2: specific to pseudogene man, comprising

SEQ No. 5 B1: 5'- tgc ata ttt att aca tcg ggg caa att -fluorescein -3'

SEQ No. 6 B2: 5'-LC Red 640- aag gca caa gag gcc cta gat ttc ta -ph -3'

45. (Amended) Hybridization probe pair C1/C2: specific to PTEN pseudogene man (C2) and homologue of pig (C1) comprising

SEQ No. 7 - C1: 5'- tgc ata ttt gtt aca tcg ggg taa att - fluorescein -3'

SEQ No. 8 - C2: corresponds to probe B2.

47. (Amended) DNA sequences of homologues of the PTEN/MMAC1 gene and/or of homologues of the PTEN/MMAC1 pseudogene, which are compiled in the annex under "list of species sequences", which as compared to the PTEN/MMAC1 gene and/or the PTEN/MMAC1 pseudogene comprise genetic variants comprising base substitutions and/or insertions and/or deletions and are suited for identifying corresponding species.

48. (Amended) A kit for carrying out the method according to claim 1, comprising:

a) one or more vessels comprising PCR and/or sequencing oligonucleotides binding to highly conserved genes, the oligonucleotides being optionally labeled radioactively or by means of a dye or in another way,

b) vessels having further common reagents for DNA amplification and/or DNA analysis,

and

c) a vessel containing a control DNA which is suited for testing the oligonucleotides and the reaction conditions.

49. (Amended) The kit according to claim 48, comprising:

a) one or more vessels with PCR and/or sequencing oligonucleotides.

50. (Amended) The kit for identifying species for carrying out the method according to claim 1, comprising:

a) a vessel having an oligonucleotide pair comprising the following sequences: 5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3' and 5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',

b) two vessels with one of the following sequencing oligonucleotides each, these oligonucleotides being optionally labeled radioactively or by means of a dye or in another way:

5'- cag gaa aca gct atg ac -3' and

5'- cga cgt tgt aaa acg acg gcc agt -3',

c) a vessel containing a control *DNA,* which is suited for testing the oligonucleotides and the reaction conditions.

51. (Amended) The kit (Light Cycler Kit) for carrying out the method according to claim 32, comprising

a) one or more vessels containing PCR primers and hybridization probes, which bind to highly conserved genes, the hybridization probes being optionally labeled by means of a dye,

b) vessels containing further common reagents for DNA amplification and/or DNA analysis,

and

c) a vessel containing a control DNA which is suited for testing the oligonucleotides and the reaction conditions.

52. (Amended) The kit (Light Cycler Kit) for carrying out the method according to claim 32, comprising:

a) one or more vessels with PCR primers and hybridization probes.

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REMARKS

Entry of the foregoing amendments is respectfully requested.

Respectfully submitted,

BURNS, DOANE, SWECKER & MATHIS, L.L.P.

By: ______________________

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Date: September 17, 2001

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Attachment to Preliminary Amendment dated XXX

Marked-up Claims 1-45 and 47-52

1. (Amended) A method of identifying organisms by comparative genetic analysis, [characterized in that] wherein the coding and/or non-coding areas and/or functionally significant areas of highly conserved genes and/or their homologous genes and/or their cDNA copies and/or their pseudogenes are amplified using PCR and are subsequently genotyped and analyzed.

2. (Amended) The method according to claim 1, [characterized in that] wherein one primer pair each is used for each specific segment of the highly conserved gene, which is located in the highly conserved exon region and/or non-coding areas and/or functionally significant areas and/or in the 5'- or 3'-untranslated area of the gene and binds in as many studied species DNAs as possible, preferable in all studied species DNAs, and enables the amplification of the corresponding gene area.

3. (Amended) The method according to [claims 1 and 2] claim 1, [characterized in that] wherein the coding and/or non-coding areas located between the primers and being either highly variant intron regions and/or variant exon regions or 5'- or 3'-untranslated areas of the gene, are analyzed as regards their sequence and identified by comparison with the species-specific sequence variants.

Attachment to Preliminary Amendment dated XXX

Marked-up Claims 1-45 and 47-52

4. (Amended) The method according to [claims 1 to 3] claim 1, [characterized in that] wherein either the sense strand or the antisense strand of any species DNA or also their PCR copies are used for the identification.

5. (Amended) The method according to [claims 1 to 4] claim 1, [characterized in that preferably] wherein animals are identified.

6. (Amended) The method according to [claims 1 to 4] claim 1, [characterized in that preferably] wherein vertebrates are identified.

7. (Amended) The method according to [claims 1 to 4] claim 1, [characterized in that preferably] wherein mammals are identified.

8. (Amended) The method according to [claims 1 to 4] claim 1, [characterized in that preferably] wherein plants are identified.

9. (Amended) The method according to [claims 1 to 4] claim 1, [characterized in that] wherein genotying is carried out by DNA sequencing, any hybridization [methods] method, restriction fragment length analyses, chromatographic methods, spectroscopic and

Attachment to Preliminary Amendment dated XXX

Marked-up Claims 1-45 and 47-52

[in particular] mass-spectroscopic methods, allele-specific PCR or by other methods suitable for detecting DNA sequence variants.

10. (Amended) The method according to [claims 1 to 4] claim 1, [characterized in that] wherein exon and/or intron areas as well as functionally significant areas of the highly conserved tumor suppressor gene PTEN/MMAC1 and its homologues are used for amplification and subsequent genetic analysis.

11. (Amended) The method according to [claims 1 to 4] claim 1, wherein cDNA copies of the PTEN/MMAC1 gene and its homologues are used for the genetic analysis.

12. (Amended) The method according to [claims 1 to 4] claim 1, wherein pseudogenes or segments of pseudogenes of the PTEN/MMAC1 gene and its homologues are used for the genetic analysis.

13. (Amended) The method according to [claims 1 to 4] claim 1, [characterized in that preferably] wherein exons arranged [side by side of] next to the PTEN/MMAC1 gene and its homologues and/or the parts of the introns following the exons are analyzed genetically.

Attachment to Preliminary Amendment dated XXX

Marked-up Claims 1-45 and 47-52

14. (Amended) The method according to [claims 1 to 4] claim 1, [characterized in that] wherein the exon regions 1 and 2 and/or 3 and 4 and/or 4 and 5 and/or 5 and 6 and/or 6 and 7 and/or 7 and 8 and/or 8 and 9 with the enclosed intron regions 1 and/or 2 and/or 3 and/or 4 and/or 5 and/or 6 and/or 7 and/or 8 as well as the 5'- and 3'-untranslated regions of the PTEN/MMAC1 gene and their homologues are used for the genetic analysis.

15. (Amended) The method according to [claims 1 to 4] claim 1, [characterized by] comprising selecting areas of highly conserved genes and/or pseudogenes and their homologues, constructing suitable oligonucleotides as primers which bind to the corresponding complementary coding and/or non-coding areas and/or functionally significant areas, amplifying them by means of a suitable technique and comparatively analyzing the sequence of the corresponding coding and/or non-coding area of various species by genetic analysis.

16. (Amended) The method according to claim 15, [characterized in that] wherein areas of the PTEN/MMAC1 gene and/or the pseudogene and their homologues are selected.

17. (Amended) The method according to [claims 15 and 16] claim 15, [characterized in that] wherein differing sequence segments of each individual exon, intron

Attachment to Preliminary Amendment dated XXX

Marked-up Claims 1-45 and 47-52

or untranslated region of the PTEN/MMAC1 gene and their homologues or the corresponding cDNA are selected.

18. (Amended) The method according to [claims 1 to 17] claim 1, [characterized in that] wherein genotyping of pig DNA which is obtained [preferably] from foodstuffs, is carried out on the basis of the gene sequence variant of PTEN/MMAC1 containing a 9-base pair long deletion.

19. (Amended) An oligonucleotide primer for the PCR and the sequencing of exon 1 and/or 5'-untranslated region of the PTEN/MMAC1 gene and its homologues, [characterized by] comprising the following sequences:

PTENex1-401 sense

5'-cccttctactgcctcca -3'

PTENex1 -465 sense

5'- gggagggggtctgagt -3'

PTENex1 ATG sense

5'- atgacagccatcatcaaaga -3'

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PTENex1 R antisense

5'- aggtcaagtctaagtcgaatc -3'

20. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 2 of the PTEN/MMAC1 gene and its homologues, [characterized by] comprising the following sequences:

PTENex2F sense

5'- atatttatccaaacattattgctat -3'

PTENex2R antisense

5'- cttactacatcatcaatattgttcc -3'

21. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 4, intron 4 and exon 5 of the PTEN/MMAC1 gene and its homologues, [characterized by] comprising the following sequences:

Zoo43sUV sense

5'- tgtgctgagagacattatgac -3'

SPL5 sense

5'- aaatttaattgcagaggt -3'

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Zoo44aRV antisense

5'- ttgtctctggtccttacttc -3'

22. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 5 of the PTEN/MMAC1 gene and its homologues, [characterized by] comprising the following sequences:

PTEN se sense

5'- atcttgaccaatggctaagtg -3'

Zoo44aRV antisense

5'- ttgtctctggtccttacttc -3'

23. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 6 of the PTEN/MMAC1 gene and its homologues, [characterized by] comprising the following sequences:

PTENex6F sense

5'- gga gta act att ccc agt cag ag -3'

PTENex6R antisense

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5'- gca agt tcc gcc act gaa -3'

24. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 7 of the PTEN/MMAC1 gene and its homologues, [characterized by] comprising the following sequences:

PTENex7F sense

5'- cct cag ttt gtg gtc tgc ca -3'

PTENex7R antisense

5'- c ctt ttt tag cat ctt gtt ctg ttt -3'

25. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 8 of the PTEN/MMAC1 gene and its homologues, [characterized by] comprising the following sequences:

PTENex8F sense

5'- caa aat gtt tca ctt ttg ggt aaa -3'

PTENex8R antisense

5'- taa aat ttg gag aaa agt atc ggt t -3'

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26. (Amended) The oligonucleotide primer for PCR and the sequencing of exon 9 of the PTEN/MMAC1 gene and its homologues, [characterized by] comprising the following sequences:

PTENex9F sense

5'- gtg aag ctg tac ttc aca aaa ac -3'

PTENex9tga antisense

5'- aaa aaa att cag act ttt gta att tg -3'

27. (Amended) The method according to [claims 1 to 17] claim 1, [characterized in that for] wherein the DNA amplification involves a mixture of oligonucleotides [is used] which differ at the 3' region of the oligonucleotide as regards its length by one or more nucleotides or which differ as regards their nucleotide sequence at the 3' end of the oligonucleotide at one or more positions.

28. (Amended) The method according to [claims 1 to 17 and 26] claim 1, wherein the oligonucleotides

sense:

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',

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5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat t -3',

antisense:

5' - cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc t -3'

are used for the amplification.

29. (Amended) The method according to [claims 1 to 17 and 26] <u>claim 1</u>, wherein the oligonucleotides

sense:

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gaa -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gag -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gat -3',

antisense:

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt a -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt g -3',

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5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt t -3'

are used for the amplification.

30. (Amended) The method according to [claims 1 to 17] claim 1, [characterized in that] wherein DNA sequencing methods are used for the genetic analysis.

31. (Amended) The method according to [claims 1 to 17] claim 1, [characterized in that] wherein DNA sequencing techniques are used in the genetic analysis for the PTEN/MMAC1 and/or its pseudogenes and their homologues.

32. (Amended) The method of distinguishing the DNA of various species, [characterized in that] wherein at least one hybridization probe pair is used, the melting points of different combinations are determined and compiled for each species into a panel.

33. (Amended) The method of distinguishing the DNA of various species, [characterized in that] wherein at least one hybridization probe pair is used and at least one gene segment is amplified, differing hybridization probe pairs hybridize to different gene segments, and the melting points of the different combinations are determined and compiled

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for each species into a panel and/or compared with this panel for the purpose of identification.

34. (Amended) The method of distinguishing the DNA of different species according to claim 33, [characterized in that] wherein at least one hybridization probe pair is used and at least one gene segment of at least one species is amplified, differing hybridization probe pairs hybridize to different gene segments of various species, and the melting points of the different combinations are determined and compiled for each species into a panel and/or compared with this panel for the purpose of identification.

35. (Amended) The method of distinguishing the DNA of various species according to [claims 33 and 34] claim 33, [characterized in that] wherein at least two hybridization probes of SEQ Nos. 3 to 8 are used, the melting points of different combinations are determined and compiled for each species into a panel.

36. (Amended) The method according to [claims 33 and 34] claim 33, [characterized in that] wherein the species differentiation of pig DNA from various other species is made using the hybridization probe pair Al/A2 as the hybridization probe pair.

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37. (Amended) The method according to [claims 33 and 34] claim 33, [characterized in that] wherein the hybridization probes are used in combinations Cl/C2; A1/B2; A1/A2; C1/A2; B1/B2; B1/A2 for the species differentiation between various species.

38. (Amended) LightCycler hybridization probes for exon 5, [characterized by] comprising the sequences:

A1: 5'- tgc ata ttt gtt tca tcc ggg caa att -fluorescein -3'

A2: 5'- LC Red 705 - tta aag gca caa gat ttc tat ggg ga - ph -3'

B1: 5'- tgc ata ttt att aca tcg ggg caa att -fluorescein -3'

B2: 5'- LC Red 640 - aag gca caa gag gcc cta gat ttc ta - ph -3'

C1: 5'-tgc ata ttt gtt aca tcg ggg taa att fluorescein -3'

C2: 5'- LC Red 640 - aag gca caa gag gcc cta gat ttc ta - ph -3'

39. (Amended) LightCycler hybridization probes for exon 6, [characterized by] comprising the sequences

PTENex6FL

5'- tca tct gga tta tag acc agt ggc act - fluorescein -3'

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PTENex6LC 640

5'- LC Red 640 - ttc aca aga tga tgt ttg aaa cta ttc caa- ph -3'

PTENex6F*

5'- gtg cca ctg gtc tat aat cca gat- fluorescein -3'

PTENex6L* 705

5'- LC Red 705- ttc ttt aac agg tag cta taa taa tac aca ta- ph -3'

40. (Amended) [The] LightCycler hybridization probes for exon 7, [characterized by] comprising the sequences

PTENex7F*

5'- taa agg tga aga tat att cct cca att ca - fluorescein -3'

PTENex7L*640

5'-LC Red 640- acc cac acg acg gga aga caa g - ph -3'

PTENex7 FL

5'-ggtaacggctgagggaactcaaagtac - fluorescein -3'

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PTENex7 LC (705-labeled)

5'-LC Red 705- tgaacttgtcttcccgtcgtgtgg- ph -3'

41. (Amended) [The] LightCycler hybridization probes for exon 8, [characterized by] comprising the following sequences

PTENex8F*

5'- tga caa gga ata tct agt act tac ttt aac aaa-fluorescein -3'

PPTENex8L* 705

5'-LC Red 705 - ctt gac aaa gca aat aaa gac aaa gc- ph -3'

PTENex8 FLU

5' - tgctatcgatttcttgatcacatagacttccatttt - fluorescein -3'

PTENex8 LCR (640-labeled)

5'-LC Red 640- actttttctgaggtttcctctggtcctggtat - ph -3'

42. (Amended) [The] LightCycler hybridization probes for exon 9, [characterized by] comprising the following sequences

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PTENex9 FL

5'-aac atc tgg tgt tac aga agt tga act gct- fluorescein -3'

PTENex9 LC 640

5'-LC-640- cct ctg gat ttg acg gct cct cta ct - ph -3'

43. (Amended) Hybridization probe pair AI/A2: specific to PTEN pseudogene pig, [characterized by] comprising

SEQ No. 3 A1: 5'- tgc ata ttt gtt tca tcc ggg caa att -fluorescein -3'

SEQ No. 4 A2: 5'-LC Red 705- tta aag gca caa gat ttc tat ggg ga - ph -3'

44. (Amended) Hybridization probe pair B1/B2: specific to pseudogene man, [characterized by] comprising

SEQ No. 5 B1: 5'- tgc ata ttt att aca tcg ggg caa att -fluorescein -3'

SEQ No. 6 B2: 5'-LC Red 640- aag gca caa gag gcc cta gat ttc ta -ph -3'

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45. (Amended) Hybridization probe pair C1/C2: specific to PTEN pseudogene man (C2) and homologue of pig (C1) [characterized by] comprising

SEQ No. 7 - C1: 5'- tgc ata ttt gtt aca tcg ggg taa att - fluorescein -3'

SEQ No. 8 - C2: corresponds to probe B2.

47. (Amended) DNA sequences of homologues of the PTEN/MMAC1 gene and/or of homologues of the PTEN/MMAC1 pseudogene, which are compiled in the annex under "list of species sequences", which as compared to the PTEN/MMAC1 gene and/or the PTEN/MMAC1 pseudogene comprise genetic variants [such as] comprising base substitutions and/or insertions and/or deletions and are suited for identifying corresponding species.

48. (Amended) A kit for carrying out the method according to [claims 1 to 18 and further claims] claim 1, comprising:

a) one or more vessels comprising PCR and/or sequencing oligonucleotides binding to highly conserved genes, the oligonucleotides being optionally labeled radioactively or by means of a dye or in another way,

b) vessels having further common reagents for DNA amplification and/or DNA analysis, [in particular for DNA sequencing,]

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and

c) a vessel containing a control DNA which is suited for testing the oligonucleotides and the reaction conditions.

49. (Amended) The kit according to claim 48 [for carrying out the method according to claims 1 to 18 and further claims], comprising:

a) one or more vessels with PCR and/or sequencing oligonucleotides [according to claims 19 to 26].

50. (Amended) [Kit] The kit for identifying species for carrying out the method according to [claims 1 to 18 and further claims] claim 1, comprising:

a) a vessel having an oligonucleotide pair comprising the following sequences: 5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3' and 5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',

b) two vessels with one of the following sequencing oligonucleotides each, these oligonucleotides being optionally labeled radioactively or by means of a dye or in another way:

5'- cag gaa aca gct atg ac -3' and

5'- cga cgt tgt aaa acg acg gcc agt -3',

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c) a vessel containing a control *DNA*, which is suited for testing the oligonucleotides and the reaction conditions.

51. (Amended) The kit (Light Cycler Kit) for carrying out the method according to [claims 32 to 37 and further claims] claim 32, comprising

a) one or more vessels containing PCR primers and hybridization probes, which bind to highly conserved genes, the hybridization probes being optionally labeled by means of a dye,

b) vessels containing further common reagents for DNA amplification and/or DNA analysis, [in particular for the Light Cycler Analyses,]

and

c) a vessel containing a control DNA which is suited for testing the oligonucleotides and the reaction conditions.

52. (Amended) The kit (Light Cycler Kit) for carrying out the method according [to claims 32 to 37 and further claims] claim 32, comprising:

a) one or more vessels with PCR primers and hybridization probes [according to claims 38 to 42].

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Method for Identifying Organisms by Means of Comparative Genetic Analysis and Primers and Hybridization Probes for Carrying out this Method

Description

The present invention relates to a method for the genetic analysis of organisms of different species of animal and/or plant by studying coding and non-coding areas of highly conserved genes or pseudogenes and their homologues with various species of animal and plant.

The known methods serving for simply, readily and precisely determining gene sequences to detect relationships and to identify organisms are based on the use of oligonucleotides which are specific to a species. These oligonucleotides are necessary to provide sufficient genetic material for the subsequent sequence reaction by means of polymerase chain reaction or other methods. An oligonucleotide is usually a short synthetically produced molecule which binds to a specific gene segment and has a specific sequence complementary to this strand. The drawback of methods based on the use of oligonucleotides consists in that gene sequences of different species usually differ strongly. In order to sequence organisms of different species, species-specific DNA sequences must, as a rule, be determined by means of methods which are costly and time-consuming, and the corresponding oligonucleotides which bind specifically to these DNA sequences must be synthesized in a second step. These two steps are usually required for each organism to be studied of unknown origin. For a subsequent analysis for determining the identity or the relationship due to the gene sequence the DNA of the organisms to be studied must then be tested with a usually large number of different oligonucleotides. Since usually only oligonucleotides of few

species are available, the analysis often fails to be a success in the case of rare species of animal. The analysis is also time-consuming and expensive.

Other methods which utilize e.g. restriction length polymorphisms of the organisms or methods used for amplifying a mixture of short oligonucleotides randomized as regards their sequence (random amplified polymorphic DNA, RAPD) do not result in an accurate and unambiguous analysis of the gene sequence of individual animals. As a result, it is difficult to determine the relationship between organisms by means of these methods.

It is thus the object of this invention to provide a method for the genetic analysis of organisms, which is highly sensitive, supplies reliable results while consuming little time, is also suited for major serial examinations and routine tests, and can optionally also be carried out automatically. The object of this invention also consists in developing means or products for carrying out this method.

The invention is realized according to the claims, the subclaims being preferred variants.

The subject matter of the invention relates to a method by which the gene sequence of a gene area of various species can be determined readily, simply and safely in a reproducible way. Three preconditions must be met here: The oligonucleotides serving as primers for the amplification of the DNA must bind to areas of the genome which are highly conserved to ensure an amplification of genetic material by means of an identical oligonucleotide pair in all or the greatest possible number of different organisms. These oligonucleotides must cover an area which has a great sequence diversity between different species to enable a differentiation. The area which is covered by the oligonucleotides used as primers should be as small as possible to maximize the yields of amplificates and to ensure that copies can also be obtained from strongly degraded DNA in the starting material.

According to the invention this object is achieved by providing a method of determining the identity or the

relationship by comparing coding and non-coding areas of highly conserved genes of pseudogenes and homologues. As a result, it is ensured that a single oligonucleotide pair binds to DNA sequences highly conserved between various species and thus enables a gene segment identical for all species to be amplified. The oligonucleotides comprise one or more gene areas having the greatest possible sequence differences between different species. The determination of the gene sequence of this highly polymorphous gene area in a subsequent reaction step enables the gene sequence to be allocated to a specific species.

Genotyping is made by sequencing or by other methods which are suited for the detection of sequence variants. This comprises genotyping methods assisted by polymerase chain reaction (PCR), such as allele-specific PCR, other genotyping methods using oligonucleotides (e.g. "dot blotting", or "Oligonucleotide Ligation Assays" (OLA)), methods using restriction enzymes, analysis of length polymorphisms and "single nucleotide polymorphisms" (SNP), analysis by means of spectroscopic methods such as "matrix-assisted laser desorption/ionization mass spectroscopy" (MALDI), chromatographic methods such as DHPLC for separating DNA strands of differing lengths and sequences and in principle any method available at present or in the future for variant detection, including DNA, RNA and PNA hybridization methods, light cycler technology, TaqMan and molecular beacon technology and the chip technology in all its technological realizations.

The following steps are preferably carried out in the method according to the invention:

a) DNA isolation: DNA is isolated and purified from blood samples, tissues, hair, foodstuffs and samples containing DNA.

b) Polymerase chain reaction: The polymerase chain reaction serves for amplifying DNA for the subsequent sequencing reaction. In the polymerase chain reaction, one or more oligonucleotide pairs bind to the DNA to be analyzed (template DNA) of genes which are highly conserved between organisms of various species. In each case, one of the

molecules of an oligonucleotide pair (sense and antisense oligonucleotide) is complementary to one of the two template DNA strands at the 5' or 3' end of a DNA sequence. The binding is oriented such that the synthesis products obtained in an oligonucleotide-controlled polymerase chain reaction using one of the two oligonucleotides each may serve, following denaturation, as a matrix for binding the respectively other oligonucleotide. The oligonucleotide pair flanks the area which shall be copied. These oligonucleotides are extended in accordance with the nucleotide sequence of the template strand by means of polymerase and following the addition of nucleotide building blocks. Binding, extension and denaturation take place at different temperatures and are usually carried out 20 to 35 times in succession so as to multiply exponentially the area covered by the oligonucleotides.

c) Agarose gel electrophoresis: The DNA fragments are separated from the oligonucleotides in an agarose gel with a voltage being applied, and the band specific to the PCR product is excised using a scalpel and purified.

d) Sequencing reaction: Another polymerase is added as well as all nucleotide building blocks and special nucleotide building blocks which terminate the chain in the extending reaction. As a result, DNA fragments form which differ in length by one nucleotide each. Areas within the gene are sequenced which as regards their gene sequence are polymorphous between the different species. Therefore, the DNA sequence characteristic of a species can be determined and allocated to a species.

e) Polyacrylamide gel eletrophoresis: If after concluding the sequencing reactions the differently long DNA strands are separated on a high-resolution polyacrylamide gel in an electric field, shorter DNA strands will migrate more rapidly than longer strands. In the pattern of bands forming, the order from shorter band to the respective band next in length – allocated to the corresponding bases A, C, G or T – corresponds to the complementary DNA sequence of the template. As a result, the sequence of the DNA strand, which was amplified by means of polymerase chain reaction

beforehand, becomes readable.

f) Comparative analysis of the gene sequence between the animal species and storage of the sequencing data.

For the amplification the method according to the invention preferably uses oligonucleotide pairs which bind to coding or non-coding areas of highly conserved genes or pseudogenes and their homologues, i.e. to genes or pseudogenes and their homologues which show no, or only minor, sequence differences between the individual species. This ensures that an amplificate can be formed in each gene segment to be analyzed of the most differing species by means of a primer pair.

The method according to the invention preferably serves for analyzing areas of the gene or pseudogene and their homologues, which differ as regards their gene sequence between organisms of different species. These may be sequences of coding or non-coding DNA.

The method according to the invention uses for certain batches for the polymerase chain reaction several differently long oligonucleotide pairs in a reaction mixture (multiplex PCR), all of which are partially identical with a starting sequence. Here, the sense or antisense oligonucleotides differ each as regards the nucleotide sequence such that the lengths of some oligonucleotides differ in the 3' region by one or more nucleotides. The use of several oligonucleotides differing in length shall ensure that binding of the oligonucleotides to the template DNA will be possible even if the template DNA differs from some oligonucleotides used as regards the 3' region. The correspondence in the 3' region of the oligonucleotides with the template DNA is essential for the specific amplification and should thus be as precise as possible in this area.

Example:

sense:

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat t -3',

antisense:

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc tta c -3',

5'- cag gaa aca gct atg act tgt ctc tgg tcc t -3'.

In another preferred embodiment of the method according to the invention, multiple oligonucleotide pairs are used in a multiplex PCR, which have equal length but differ at one or more positions of the 3' end of the oligonucleotides as regards their nucleotide sequence. The use of a reaction mixture of several oligonucleotides differing as regards the base sequence at the 3' end of the oligonucleotide shall ensure that an amplificate can be formed in the most different species by means of a primer pair.

The method according to the invention preferably analyzes segments of the gene or pseudogene and their homologues which differ as regards their gene sequence between organisms of different species. These may be sequences of coding or non-coding DNA.

The method according to the invention uses for certain batches for the polymerase chain reaction several differently long oligonucleotide pairs in a reaction mixture (multiplex PCR), all of which are partially identical with a starting sequence. Here, the sense or antisense oligonucleotides differ each as regards the nucleotide sequence such that the lengths of some oligonucleotides differ in the 3' region by one or more nucleotides. The use of several oligonucleotides differing in length shall ensure that binding of the oligonucleotides to the template DNA will be possible even if the template DNA differs from some oligonucleotides used as regards the 3' region. The correspondence in the 3' region of the oligonucleotides with the template DNA is essential for the specific amplification and should thus be as precise as possible in this area.

Example

sense:

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat

-3',
5' - cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat t
-3',
antisense:
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta c -3',
5'- cag gaa aca gct atg act tgt ctc tgg tcc t -3'.

In another preferred embodiment, the method according to the invention uses multiple oligonucleotide pairs in a multiplex PCR, which have equal length but differ at one or more positions of the 3' end of the oligonucleotides as regards the nucleotide sequence. The use of a reaction mixture of several oligonucleotides differing as regards the 3' end of the oligonucleotide shall ensure that the oligonucleotides are bound to the template DNA even if the template DNA differs at the 3' binding site of the oligonucleotide from the usually used oligonucleotide. For this purpose, a mixture of different oligonucleotides which have all conceivable nucleotide sequences at their 3' end is provided for the amplification.

Example:

sense:
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gaa -3',
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gag -3',
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gat -3',
antisense:
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt a -3',
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt g -3',
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt t -3'.

When suitable oligonucleotide sequences are selected, the method according to the invention pays attention to the fact that as many oligonucleotides as possible correspond at their 3' end with the first nucleotide of the codon which codes for

the highly conserved amino acid. It follows from theoretical considerations and also on the basis of observations that every second nucleotide has within a codon a degree of correspondence between organisms of differing species higher than that of the first or third nucleotide of the codon. Since the amplification will usually only function if along with other preconditions the nucleotide located at the 3' end of the oligonucleotide is exactly complementary to the opposite nucleotide of the template DNA strand - i.e. A faces T or G faces C -, the sequence of the oligonucleotides employed is chosen such that the last nucleotide at the 3' end of the oligonucleotide binds, if possible, to the most highly conserved nucleotide of the codon coding for an amino acid.

The method according to the invention preferably uses for different segments of the gene, of the pseudogenes and its homologues a single oligonucleotide pair each, which binds to the highly conserved tumor suppressor gene PTEN/MMAC1, its pseudogene and their homologues in different species, namely in the area of the gene which shows major correspondence between the species [Steck *et al.*, 1997]. This area concerns the entire coding sequence of the gene, pseudogene and its homologues as well as exon-intron transitions and 5'- and 3'-untranslated regions of the gene, pseudogene and their homologues.

The areas amplified by means of the above described methods comprise sequence segments which have more or less great sequence differences between the individual species. This applies in particular to intron regions and specifically to intron 4. The oligonucleotide pair used for the amplification may bind to exons 4 and 5, since the PTEN/MMAC1 gene, pseudogene and their homologues show no, or only slight, differences between the species in exon 4 and exon 5. The intron region 4 covered by both oligonucleotides, which in contrast to the exon regions 4 and 5 between the species has considerably greater sequence differences, is amplified. Thereafter, part of this intron region is sequenced preferably by means of a sequencing reaction (see figure 1).

By means of comparative analyses, it is possible to determine due to the correspondence of intron sequences whether different samples belong to an identical species. It is also possible to determine the relationship of different species by means of comparative analysis of an intron region comprising only some to several hundred bases of the PTEN/MMAC1 gene and its homologues due to the similarity of the sequences. The general rule is that for the differentiation of closely related species the intron segments which must be studied have to be longer than those of distantly related species. This procedure described for exons 4/5 and intron 4 may also be applied to all of the other introns enclosed by exons. It also applies to pure exon regions, pseudogenes and the 5'- and 3'-untranslated regions as well as their homologues, in these cases the sequence differences between the individual species being less than in the intron regions.

In a preferred embodiment of the method according to the invention, highly conserved pseudogenes and their homologues are studied in various organisms and used for determining the species-specific gene sequence. These pseudogenes and their homologues have the advantage that they are also highly conserved as regards their nucleotide sequence and allow an amplification in certain species. However, the sequence differs in some areas of the pseudogene and its homologues between different species, so that pseudogenes and their homologues can be used for the species-specific characterization of organisms. Since the intron regions lack, they - like pure exon regions and the 5'- and 3'-untranslated regions - are suitable for the analysis, in particular of DNA degraded due to environmental influences, because of the small size.

An advantageous execution of the method utilizes the deletion identified by inventors and having a length of 9 base pairs in a PCR product (see figure 3 and Example 2), which corresponds to a gene sequence variant of PTEN/MMAC1 and was amplified from DNA of pig cells. This deletion having a

length of 9 base pairs is typically found in domestic pigs and all examined wild boars and as for the rest in no other examined species. In a variant of an embodiment of the invention this difference in length serves for proving pig meat in foodstuffs. This variant in length is genotyped by sequencing or by other methods suitable for detecting this deletion. They comprise PCR-assisted genotyping methods such as PCR by means of species-specific oligonucleotides, hybridization techniques such as the light cycler technology or other genotyping methods using restriction enzymes, and in principle any method available at present or in the future for detecting variants, including the chip technology and all of their technological realizations. Deletions and insertions, as found in different species in intron 4, exon 8 and in the 5'-untranslated region, can also be used correspondingly for identifying species (see annex: "List of species sequences").

The method according to the invention was made with DNA from different species as a model system and the gene sequence in the area of two segments in intron 4 of the PTEN/MMAC1 gene and its homologues was determined. It was possible to amplify all species with only one oligonucleotide pair. In the sequencing reaction with only one oligonucleotide and in the subsequent analytical polyacrylamide gel electrophoreses it turned out that all investigated species differ as regards the nucleotide sequence in the intron region (see annex: "List of species sequences"). Since the PTEN/MMAC1 tumor suppressor gene and its pseudogene and their homologues are conserved, the method can in other species also amplify successfully the corresponding gene sequences of lower organisms and possibly plants by means of an oligonucleotide pair. The method according to the invention is thus suited to determine the identity and relationship of various organisms. A data library was established which can be used for identifying different species and humans. It comprises PCR primers, sequencing primers and hybridization probes as well as sequences of the coding and non-coding areas including select highly variant intron regions, of exon regions, of the

5'-untranslated region of the gene and its homologues as well as of the pseudogene and its homologues from the most differing vertebrates (see annex: "List of species sequences"). On the one hand, the method according to the invention is suited to determine readily, simply and safely in a reproducible manner the relationship in certain species which are clearly classified (phylogenetic analyses). On the other hand, it is possible to determine by a comparison with gene sequences which can clearly be allocated to a species, the identity of tissue samples, blood samples and foodstuffs and all samples which contain DNA and are of unknown origin. Therefore, the method is also suited for applications in forensic medicine. Since in a preferred embodiment of the method according to the invention DNA is used as the starting material, organic samples (e.g. blood, saliva, tissue residues) can clearly be allocated to human or animal origin because of their gene sequence. Due to the possibility of comparing the collected DNA sequence with an already established data library with DNA sequences of known species it is possible to make statements on the species. If the gene sequence is unknown, it is possible due to sequence similarities to make statements on the relationship which the species to be studied has with a comparative DNA.

An advantageous embodiment of the invention utilizes hybridization probes for distinguishing the DNAs of various species among one another. This method uses differing ways for distinguishing the species on the basis of the LightCycler analysis system (company of Roche Molecular Biochemicals) using hybridization probes (patents WO 97/46714; WO 97/39008).

The LightCycler analysis system makes possible the amplification, detection and specific analysis of DNA of differing species and their differentiation within the shortest possible time and with moderate expenditure. The LightCycler is a micro-volume fluorimeter having a thermocycler combining rapid thermocycling with real-time fluorescence observation during the PCR (Wittwer *et al.*, 1997a). By means of this technology, the time for the

amplification and the detection of nucleic acids is reduced from about 5 hours to about 30 minutes. For a specific detection during the PCR reaction, the synthesis can be observed on the basis of the fluorescence resonance energy transfer (FRET) via two adjacent hybridization probes labeled with fluorescent dyes. Here, one probe is labeled at its 3' end with a donor fluorophore (usually fluorescein) and the adjacent probe is labeled at its 5' end with an acceptor fluorophore. During FRET, the donor dye is excited by an external light source and emits light which is absorbed by the acceptor fluororphore. The latter in turn emits light having another wavelength which is measured specifically. This FRET can only be made if both probes hybridize side by side within the amplification pair at a distance of about 1-5 bp, on the target DNA. Here, the sequence of the probes is selected such that it is complementary to the target area [Wittwer *et al.* 1997b; Lay, 1997, Bernard, 1998; Ririe, 1997; Bernard, 1999; Nauck, 1999a; Nauck, 1999b, Kreuzer, 1999; Kyger, 1998; Mangasser-Stephan, 1999; Aslandis, 1999].

In order to detect the specific amplification product and to differentiate differences in the target sequence, the LightCycler provides the possibility of carrying out melting point analyses. The melting point analysis is based on the fact that two complementary DNA strands are separated at a characteristic temperature, the melting temperature, into two individual strands. This melting temperature depends on the base composition in which sequences rich in GC have a higher melting point than sequences with predominantly AT bases. If a melting point analysis is carried out by removing more or less well complementary hybridization probes from the template DNA under certain temperature conditions, there is a melting profile characteristic of the fitting between probe and target sequence to be analyzed in the form of a fluorescence intensity measurement. As a result, the changes in the target sequence can be detected. If the sequences are fully complementary to one another, the probes will fully hybridize. If the target sequence contains changes in its base sequence, the melting point of the probes is lowered

correspondingly. Due to a continuous detection of the fluorescence up to the melting of the probes, a melting curve can be prepared for each sample in the form of the fluorescence intensity as a function of the temperature. A comparison of the melting peaks made by the first negative derivative of the fluorescence to the temperature (-dF/dt vs T) enables a verification and differentiation of various DNAs. Fragments having a lower or higher melting temperature can be distinguished clearly.

In particularly preferred variants of embodiments of the invention, oligonucleotide pairs were found for the polymerase chain reaction (PCR) which bind to the highly conserved tumor suppressor gene PTEN/MMAC1, its pseudogene and their homologues in areas which show large correspondence between the species. These are usually exon regions or untranslated areas of the 3' and 5' ends of the gene, its pseudogene and their homologues.

These oligonucleotide pairs allow to amplify small gene segments containing areas which have differing base sequences between the individual species, including base substitutions, base deletions and base insertions. Examples 4, 5 and 6 use a 9-base pair deletion of the pig homologue of the PTEN/MMAC1 pseudogene and numerous further sequence variants of the gene, pseudogene and their homologues in various species to produce by means of specific hybridization probes differing melting profiles with differing species, which clearly distinguish the species from one another. This preferred area of Examples 4 to 6 relates exclusively to exon 5 of the gene, pseudogene and their homologues. The PCR primers used for the amplification of the corresponding gene segment read as follows:

Sense primer: PTEN se 5'- atc ttg acc aat ggc taa gtg -3'
Antisense primer: Zoo44aRV 5'- ttgt ctc tgg tcc tta ctt c -3'

Hybridization probes according to the invention were selected on the one hand with the target area of the 9-base pair deletion of the pig pseudogene. Probe A1/A2 enables a

distinction of the pig DNA from all of the other species.

Since by the above PCR primer pair, it is not only the pseudogene but also the gene area of exon 5 of the pig homologue of PTEN/MMAC1 that is amplified, another probe pair was provided with the complementary sequence of the pig homologue. This is probe C1/C2.

Since the different species in this gene area show minor sequence differences which should be used for a detailed differentiation among one another, a third probe pair which corresponds to the sequence of the human pseudogene in the selected area was constructed (probe B1/B2).

According to the invention, the probes A1/A2 are concerned: specific to PTEN pseudogene pig:
A1: 5'- tgc ata ttt gtt tca tcc ggg caa att - fluorescein -3'
A2: 5'- LC Red 705 - tta aag gca caa gat ttc tat ggg ga - ph -3'

Probes B1/B2: specific to PTEN pseudogene man:
B1: 5'- tgc ata ttt att aca tcg ggg caa att - fluorescein -3'
B2: 5'- LC Red 640 - aag gca caa gag gcc cta gat ttc ta - ph -3'

Probes C1/C2: specific to PTEN homologue pig:
C1: 5'- tgc ata ttt gtt aca tcg ggg taa att - fluorescein -3'
C2: corresponds to probe B2

The positions of probes A1, A2, B1, B2, C1 and C2 in exon 5 are shown in figure 4.

The separate use of these three probe pairs and the use of the probes in various possible combinations (1 donor dye + 1 acceptor dye) yields for each individual species a characteristic panel of differing melting points enabling a clear distinction between the species (see figures 5 and 7).

The use of these hybridization probe combinations also permits to carry out studies in reaction mixtures of two or more different species.

A parallel analysis/detection of the fluorescence of two different wavelengths (640 nm and 705 nm) is possible in a multiplex reaction with two different probe pairs such that the respective donor probes are labeled differently. The acceptor probes may be identical or differ as regards their sequence. Having concluded the melting point analysis, a melting point specific to the corresponding probe and the target sequence covered by it is obtained for each of the two wavelengths.

The alternative combination from two different donor probes and one acceptor probe of one wavelength yields for a reaction mixture of two different species having minor sequence differences in the target area two melting points within one wavelength.

In general, the following general multiplex reaction batches are possible which are characterized in that at least one hybridization probe pair is used and at least one gene segment is amplified, differing hybridization probe pairs hybridize to differing gene segments, and the melting points of the different combinations are determined and compiled for each species into a panel or used for the identification.
These general multiplex reaction batches can also be characterized in that not only at least one hybridization probe pair is used and not only at least one gene segment is amplified but also DNA of at least one species is used and thus different hybridization probe pairs hybridize to differing gene segments of different species, and the melting points of the different combinations are determined and compiled for each species into a panel or used for the identification.

On this basis, the following analytical approaches are possible, melting point overlaps having to be avoided.

a) Analysis of an unknown species sample with two different donor probes and one acceptor probe of one wavelength or of differing wavelengths,
b) Analysis of two or more unknown species samples with two different donor probes and one acceptor probes of one wavelength or of different wavelengths,
c) analysis of an unknown species sample with a mixture of two or more donor probes and acceptor probes each,
d) analysis of a mixture of unknown species samples with one donor probe and one acceptor probe,
e) analysis of a mixture of unknown species samples with two or more different donor probes and two or more acceptor probes of one or more different wavelengths.

This procedure can be applied to all highly conserved segments of the PTEN/MMAC1 gene, pseudogene and their homologues and also to other highly conserved genes when species shall be distinguished.

Select primers for the amplification are defined in claims 18 to 25 and select hybridization probe sequences for the LightCycler application are defined in claims 34 to 42 for different exons of the PTEN/MMAC1 gene, pseudogene and their homologues. Due to the high conservation of the gene in the evolution, primers and hybridzation probes are also possible in all of the other conceivable areas of the gene, pseudogene and their homologues which can be used according to the above described principle for distinguishing species.

These probes and/or primers can be combined as desired in accordance with the multiplex principle with the aim of differentiating species.

The general rule is that all of the described methods and all methods conceivable at present and in the future for analyzing the DNA sequence variants can be applied to both the sense strand and antisense strand. This equivalence principle also applies to all PCR, sequence primer and hybridization probes which are described in this patent

application and the described gene sequences of the individual species of animal.

The following examples shall explain the invention in more detail.

Example 1

In this experiment, the sequence diversity between human DNA and elephant DNA is determined. The arrangement shown in figure 1 was chosen. The comparative sequence analysis was carried out by determining the species-specific sequences of intron 4 of the tumor suppressor gene PTEN/MMAC1 and its homologues. An oligonucleotide pair which is specific to areas within exons 4 and 5 of the DNA sequence of this gene for mice was chosen and subsequently synthesized (company of Amersham Pharmacia).

Oligonucleotide 1: 5'- <u>cga cgt tgt aaa acg acg gcc agt</u> tgt gct gag aga cat tat gac -3'
Oligonucleotide 2: 5'- <u>cag gaa aca gct atg act</u> tgt ctc tgg tcc tta ctt c -3'

The oligonucleotides for the polymerase chain reaction were constructed such that they have one sequence each at their 5' end (underlined) which is complementary to the two oligonucleotide used for the sequencing reaction. As a result, it is ensured that the specific oligonucleotide parts bind in each case specifically to the template DNA (not underlined) but the oligonucleotides used for sequencing may differ from those used for the polymerase chain reaction, which adds quite generally to the quality of the sequencing reaction. The specific portion of the oligonucleotides binds in each case to exon 4 and exon 5 of the PTEN/MMAC1 tumor suppressor gene and its homologues.

A veterinarian provided 3 ml of residual blood of an African elephant resulting from a routine operation. The DNAs from elephant blood and from human blood were isolated by means of the QIAgen kit (QIAGen company) in accordance with the protocols from the manufacturer and stored at -20°C until they were used.

In order to generate sufficient amounts of DNA for the sequencing reaction, a polymerase chain reaction (PCR) was carried out. 3 sample batches were provided and the following

volumes and final concentrations or amounts of substrates and units of polymerase were used: reaction vessel 1: elephant DNA 1 µl (50 ng); reaction vessel 2: human DNA 1 µl (50 ng); reaction vessel 3: no DNA but 1 µl distilled water instead (negative control). All sample batches were provided with the following: 14.35 µl distilled water; dNTPs (Promega company): 4 µl (200 µl); $MgCl_2$ (InViTek): 1 µl (2 mM); 10 x buffer (InViTek) consisting of 160 mM $(NH_4)_2SO_4$, 500 mM Tris-HCl, pH 8.8, 0.1 % Tween 20: 2.5 µl; oligonucleotides 1 and 2: 1 µl (0.2 µM); Taq polymerase (InViTek): 0.15 µl (0.75 units).
All in all, 35 cycles were carried out in a Perkin Elmer Thermocycler 9600, denaturing taking place at 94°C for 50 seconds each, the oligonucleotides binding to the DNA strands at 53°C for 50 second, and extension taking place at 72°C for 60 seconds (one second longer per cycle). Before the first cycle was started, denaturing was carried out at 94°C for 3 minutes, and a last extension phase of 10 minutes at 72°C was carried out after the last cycle.
In order to check the success of the PCR, to isolate the amplified DNA and check the negative control, an agarose gel electrophoresis was carried out: A 0.8 % agarose gel was produced by adding ethidium bromide, and 1 x TAE buffer was added. 13 µl PCR product each was added by pipetting to prepared sample bags or pockets to the gel matrix by adding 2 µl dye and a voltage of 100 V was applied. Electrophoresis was stopped after 20 to 30 minutes, the DNA bands were made visible under a U.V. lamp and thereafter excised using a scalpel. The purification of the PCR product was possible by placing the excised bands on MicroSpin columns (Amersham Pharmacia) and centrifugation at 1020 g for 10 minutes. The eluate was diluted depending on the strength of the band on the agarose gel with up to 30 µl distilled water.

The purified PCR products were subjected to a cycle sequencing reaction using oligonucleotides having the sequence 5' - Cy-5- cag gaa aca gct atg ac -3'. The oligonucleotides were labeled at the 5' end with the dye Cy-5. 4 reaction vessels (A, C, G, T) were provided per PCR

product, and the following volumes and concentrations were chosen: 3 μl PCR product each per A, C, G, T; 1 μl each per A, C, G, T reagent (Amersham Pharmacia) consisting of Tris-HCl (pH 9.5), $MgCl_2$, Tween 20, Nonidet P-40, 2-mercaptoethanol, dATP, dCTP, 7-deaza-dGTP, dTTP, thermoresistant pyrophosphatase and thermo sequenase DNA polymerase, reaction vessels A, C, G and T containing correspondingly ddATP, ddCTG, ddGTP and ddTTP. Thereafter, 1 μl oligonucleotide of the above mentioned sequence (0.5 μM) is added. The following reaction conditions were chosen: All in all, 25 cycles were carried out in a Perkin Elmer Thermocycler 9600 (Perkin Elmer company), denaturing taking place at 94°C for 20 seconds each, the oligonucleotides binding to the amplificate at 54°C for 30 seconds, and the DNA strands being extended while raising the temperature to the denaturing temperature. Prior to the commencement of the first cycle, denaturing was carried out at 94°C for 3 minutes and 30 seconds, and the last extension phase of 5 minutes was carried out at 72°C after the last cycle.

In order to make visible the sequence, the products were separated on a polyacrylamide gel in an electric field. For this purpose, the automatic laser fluorescence detection system A.L.F.express from the company of Amersham Pharmacia was chosen. The gel matrix was composed of 16.8 g urea (Gibco BRL), 5.2 ml 50 % long ranger gel solution (FMC company) and 4 ml 10 x TBE (Gibco BRL), which were diluted using distilled water to give 40 ml. The gel was polymerized by adding 140 μl 10 % APS (Merck company) and 20 μl TEMED (Serva company). 5 μl formamide loading dye were added to each reaction vessel A, C, G, T, and added by pipetting to the prepared sample pockets. The following electrophoresis conditions were chosen: 1000 V, 40 mA, 40 W.

Following the gel electrophoresis, the sequences were generated by the A.L.F.express system (Amersham Pharmacia) and could then be compared with one another. Figure 2 shows the determined nucleotide sequence differences. A comparison of the sequences between elephant DNA and human DNA in the exon region yielded a great correspondence and served as a

control for the PTEN/MMAC1 specificity, whereas the intron region differed greatly.

Example 2

In this experiment, the sequence of a pig liver provided by a butcher's is compared with already available DNA of a pig. Beef salami served as a control. DNAs were obtained from 50 to 60 mg pig liver and 50 to 60 mg beef salami using the QIAgen kit (QIAGen) and purified. For the comparative analysis, the procedure carried out in Example 1 was chosen using oligonucleotides 1 and 2 for the polymerase chain reaction. A band having a length of about 300 bp was excised from the agarose gel for the sequence analysis. This band corresponds in length to the PTEN/MMAC1 pseudogene. After purifying the excised amplificate, Cy-5-labeled oligonucleotides with the sequence 5'- Cy-5- cag gaa aca gct atg ac - 3' were sequenced. The comparative analysis of pig liver from a butcher's with pig DNA already sequenced in this area resulted in a full correspondence. The control DNA (beef salami) has a sequence markedly differing from the pig DNA (see figure 3).

Example 3

The PCR and sequencing of exons 1 to 9 is carried out with the primers described in claims 19 to 26 with otherwise analogous reaction control. The corresponding sequences of the studied species are listed in the annex under "List of species sequences".

Example 4

This experiment is to show the species differentiation between pig DNA and human DNA using various combinations of hybridization probe pairs. The comparative analysis was made by determining the melting points of the hybridization probe pairs C1+B2, A1+B2, A1+A2, and C1+A2 in pig DNA and human DNA. The probes were chosen correspondingly and synthesized

(Tib Mol Biol, Berlin.
Probes:

A1: 5'- tgc ata ttt gtt tca tcc ggg caa att - fluorescein -3'
A2: 5'- LC Red 705 - tta aag gca caa gat ttc tat ggg ga - ph - 3'

B1: 5'- tgc ata ttt att aca tcg ggg caa att - fluorescein - 3'
B2: 5'- LC Red 640 - aag gca caa gag gcc cta gat ttc ta - ph -3'

C1: 5'- tgc ata ttt gtt aca tcg ggg taa att - fluorescein - -3'
C2: 5'- LC Red 640 - aag gca caa gag gcc cta gat ttc ta - ph -3'

A precondition for a probe hybridization is the amplification of the target area with a suitable primer pair. For this purpose, the following primer pair was chosen and synthesized:

Sense primer: PTEN se 5'- atc ttg acc aat ggc taa gtg -3' (Tib Mol Biol)
Antisense primer: Zoo44aRV 5'- ttgt ctc tgg tcc tta ctt c-3' (Amersham Pharmacia)

Both primers bind to areas of the exon 5 of the PTEN/MMAC1 gene, pseudogene and their homologues, which comprises the target regions of about 172 base pairs.
The DNAs were isolated by means of the Quiagen kit (QIAGen) from the blood of pigs and humans in accordance with the protocols of the manufacturer and stored at -20°C until they were used.
The real time PCR with hybridization probes and subsequent melting point analysis was carried out as follows: 3 rows with 4 sample batches each (glass capillary cuvette (Roche)) were provided in a cooled pipetting block (Roche). In row 1,

2 μl (50 ng) pig DNA are supplied in each batch, 2 μl (50 ng) human DNA are supplied to each batch of the 2[nd] row, and 2 μl distilled water are supplied in row 3 for the negative controls. The hybridization probes were used for the corresponding batches in the following combinations: 1[st] batch of each row: A1, 1 μl (0.1 μM) and A2, 2 μl (0.2 μM); 2[nd] batch of each row: C1, 1 μl (0.1 μM) and B2, 2 μl (0.2 μM); 3[rd] batch of each row: A1, 1 μl (0.1 μM) and B2, 2 μl (0.2 μM); 4[th] batch of each row: C1, 1 μl (0.1 μM) and A2, 2 μl (0.2 μM).

The following volumes and final concentrations or amounts of substrates and units of polymerase were used in all sample batches: oligonucleotides PTEN se and Zoo44aRV 2 μl (10 μM) each; $MgCl_2$ (Roche Molecular Diagnostics): 2.4 μl (4 mM); LightCycler DNA Master Hybridization Probes (Roche Molecular Diagnostics): 2 μl of a stock solution concentrated by 10 times from Taq DNA polymerase, reaction buffer, dNTP mixture and 10 mM $MgCl_2$. The final $MgCl_2$ concentration in the total reaction batch of 20 μl is 5 mM. After fully loading all reagents, the glass capillary cuvettes are closed, centrifuged at 2000 g for 1 minute and inserted in the reaction carrousel of the LightCycler provided for the capillaries.

All in all, 45 cycles are carried out in the LightCycler analysis system as follows: denaturation at 95°C for 1 second, binding of the oligonucleotides and probes at 54°C for 10 seconds and extension of the DNA strands at 72°C for 5 seconds. Denaturation was carried out at 95°C for 30 seconds before the first cycle started. The preliminary heating rate is programmed from denaturation to binding to 20°C/second, from binding to the extension of the DNA strands to 20°C/second and for the step of extension up to the denaturation to 20°C/second. The fluorescence resulting from the FRET of the probes binding complementarily side by side, is measured for observing the PCR at the end of the binding phase in each cycle. Probes which cannot bind fully to the target DNA due to sequence differences, since their binding temperature is below that of the oligonucleotides, cannot yet

be detected at that stage of fluorescence measurement.
After the complete amplification, a melting curve was finally recorded as follows: denaturation of the amplification products at 95°C for 5 seconds, cooling to 30°C with a preliminary heating rate of 20°C/second, holding of this temperature for 15 seconds and subsequent slow heating of 0.2°C/second up to 95°C. The fluorescence of the bound hybridization probes is recorded continuously up to the respective melting/dissociation during the slow temperature increase. A melting curve is recorded for each sample by recording the fluorescence signal as a function of the temperature. By forming the first negative derivative of the fluorescence against the temperature, the melting curves are converted into melting peaks.
After balancing the fluorescence signals at 640 nm and 705 nm against the standard curves prepared with a colorcompensation kit (Roche Molecular Diagnostics) for the respective wavelength, the melting points of pig DNA could be compared with those of the human DNA for the various probe combinations. In this connection, 2 melting points each could be recorded for the pig DNA for each probe pair, and one could be recorded each for the pseudogene and one for the gene. All melting points of the pig DNA differed from those of the human DNA (figure 5).

Example 5

In this experiment, the species differentiation of pig DNA from various other species of animal is shown by means of a single hybridization probe pair. For this purpose, DNAs from cattle, sheep, dwarf goat, chicken and turkey were used for the analysis (gene sequences in the annex "list of species sequences" under "sequences intron 4 exon 5").
The comparative analysis was carried out by determining the melting points of a hybridization probe pair whose sequences are specific to the pseudogene of pigs in the area of the 9 base pair deletion (A1/A2) and which was already used in Example 4. The primers used in Example 4 were employed for

the amplification. The DNA was collected from the bloods of said species by means of the QIAGen kit (QIAGen) and purified. For the real-time PCR a sample batch having 2 μl (50 ng) of the corresponding DNA each is supplied for each species and a sample batch with 2 μl distilled water is supplied for a negative control. Furthermore, 1 μl (1 μM) of the probe A1 and 2 μl (0.2 μM) of probe A2 were added by pipetting to each sample batch. To pipette further reagents the procedure of Example 1 was chosen as regards their volumes and concentrations and for the further reaction steps at the LightCycler.
A comparison of the melting points of pig DNA with those of the other animal species shows a clear distinction between pig DNA and those of other animal species (figure 6).

Example 6

In this experiment, the species differentiation between various animal species is shown by way of the following species with hybridization probes of Example 4:
Pig, deer, dog, Indian elephant, trout, quail, duck, goitred gazelle, mouse, guinea pig (gene sequences in the annex "list of species sequences" under "sequences intron4 exon5")

A comparative analysis was carried out by determining the melting points from various combinations of the hybridization probes from Example 4 in the combinations C1+B2, A1+B2, A1+A2, C1+A2, B1+B2 and B1+A2 and compiling a panel for each species of animal.

The DNA was obtained from the bloods of said species using the QIAGen kit (QIAGen) and purified. The primers listed in Example 4 were used for the amplification. For the further course of the experiment and the subsequent melting point analysis, the procedure in Example 4 was chosen, complemented by the additional probe combinations and greater numbers of species.
A panel of their melting points was compiled for the

corresponding probe combinations for each species (figure 7). A comparison of the panels of the different species yields a difference of each species from the others results as regards at least one melting point.

Figure 8 shows the mean value curves which were determined for selected probe combinations (C1+C2/A1+A2/B1+A2 and A1+C2 from 15 pig DNAs each and C1+C2/A1+A2/B1+A2 and C1+A2 from 15 human DNAs each) with the corresponding standard deviations. The experiment control corresponds to Example 4.

Furthermore, the sequences of the investigated species for exons 1-9 and the 5'-untranslated region of the PTEN/MMAC1 gene, pseudogene and their homologues are listed in the annex under "list of species sequences".

These examples for various probe combination panels can be enlarged by any number of probes and primers for the described gene PTEN/MMAC1, pseudogene and their homologues, but also for all of the other genes, and applied. A linear increase of the primers and probe combinations in the entire genome yields an exponential growth of differentiation possibilities of the most varying species among one another. By using sequence-specific probes and several and/or any number of probe combinations, a species can be distinguished from all of the other species by its very specific melting point panel.

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Annex

List - figures 1 - 8:

Figure 1: diagram of the method for identifying organisms according to Example 1

Figure 2: comparison of the determined sequences from man and African elephant according to Example 1

Figure 3: DNA sequence comparison of a pig with purchased pig liver and beef salami according to Example 2. The differences between the nucleotide sequences are shown. The 9-base pair long deletion (nucleotides 216-224) is striking in pig / pig liver.

Figure 4: positions of the hybridization probes in exon 5 of the PTEN gene, pseudogene and their homologues

Figure 5: Example 4 - melting point panels of pig and man

Figure 6: Example 5 - melting points of the probe combination A1 + A2 in pig as compared to various species

Figure 7: Example 6 - melting point panel of various species

Figure 8: standard deviations of select probes for pig (HS) and man (WT)

Claims

1. A method of identifying organisms by comparative genetic analysis, characterized in that coding and/or non-coding areas and/or functionally significant areas of highly conserved genes and/or their homologous genes and/or their cDNA copies and/or their pseudogenes are amplified using PCR and are subsequently genotyped and analyzed.

2. The method according to claim 1, characterized in that one primer pair each is used for each specific segment of the highly conserved gene, which is located in the highly conserved exon region and/or non-coding areas and/or functionally significant areas and/or in the 5'- or 3'-untranslated area of the gene and binds in as many studied species DNAs as possible, preferable in all studied species DNAs, and enables the amplification of the corresponding gene area.

3. The method according to claims 1 and 2, characterized in that coding and/or non-coding areas located between the primers and being either highly variant intron regions and/or variant exon regions or 5'- or 3'-untranslated areas of the gene, are analyzed as regards their sequence and identified by comparison with the species-specific sequence variants.

4. The method according to claims 1 to 3, characterized in that either the sense strand or the antisense strand of any species DNA or also their PCR copies are used for the identification.

5. The method according to claims 1 to 4, characterized in that preferably animals are identified.

6. The method according to claims 1 to 4, characterized in that preferably vertebrates are identified.

7. The method according to claims 1 to 4, characterized in

that preferably mammals are identified.

8. The method according to claims 1 to 4, characterized in that preferably plants are identified.

9. The method according to claims 1 to 4, characterized in that genotying is carried out by DNA sequencing, any hybridization methods, restriction fragment length analyses, chromatographic methods, spectroscopic and in particular mass-spectroscopic methods, allele-specific PCR or by other methods suitable for detecting DNA sequence variants.

10. The method according to claims 1 to 4, characterized in that exon and/or intron areas as well as functionally significant areas of the highly conserved tumor suppressor gene PTEN/MMAC1 and its homologues are used for amplification and subsequent genetic analysis.

11. The method according to claims 1 to 4, wherein cDNA copies of the PTEN/MMAC1 gene and its homologues are used for the genetic analysis.

12. The method according to claims 1 to 4, wherein pseudogenes or segments of pseudogenes of the PTEN/MMAC1 gene and its homologues are used for the genetic analysis.

13. The method according to claims 1 to 4, characterized in that preferably exons arranged side by side of the PTEN/MMAC1 gene and its homologues and/or the parts of the introns following the exons are analyzed genetically.

14. The method according to claims 1 to 4, characterized in that the exon regions 1 and 2 and/or 3 and 4 and/or 4 and 5 and/or 5 and 6 and/or 6 and 7 and/or 7 and 8 and/or 8 and 9 with the enclosed intron regions 1 and/or 2 and/or 3 and/or 4 and/or 5 and/or 6 and/or 7 and/or 8

as well as the 5'- and 3'-untranslated regions of the PTEN/MMAC1 gene and their homologues are used for the genetic analysis.

15. The method according to claims 1 to 4, characterized by selecting areas of highly conserved genes and/or pseudogenes and their homologues, constructing suitable oligonucleotides as primers which bind to the corresponding complementary coding and/or non-coding areas and/or functionally significant areas, amplifying them by means of a suitable technique and comparatively analyzing the sequence of the corresponding coding and/or non-coding area of various species by genetic analysis.

16. The method according to claim 15, characterized in that areas of the PTEN/MMAC1 gene and/or the pseudogene and their homologues are selected.

17. The method according to claims 15 and 16, characterized in that differing sequence segments of each individual exon, intron or untranslated region of the PTEN/MMAC1 gene and their homologues or the corresponding cDNA are selected.

18. The method according to claims 1 to 17, characterized in that genotyping of pig DNA which is obtained preferably from foodstuffs, is carried out on the basis of the gene sequence variant of PTEN/MMAC1 containing a 9-base pair long deletion.

19. An oligonucleotide primer for the PCR and the sequencing of exon 1 and/or 5'-untranslated region of the PTEN/MMAC1 gene and its homologues, characterized by the following sequences:

PTENex1-401 sense
5'-cccttctactgcctcca -3'

PTENex1 -465 sense
5'- gggagggggtctgagt -3'

PTENex1 ATG sense
5'- atgacagccatcatcaaaga -3'

PTENex1 R antisense
5'- aggtcaagtctaagtcgaatc -3'

20. The oligonucleotide primer for PCR and the sequencing of exon 2 of the PTEN/MMAC1 gene and its homologues, characterized by the following sequences:

PTENex2F sense
5'- atatttatccaaacattattgctat -3'

PTENex2R antisense
5'- cttactacatcatcaatattgttcc -3'

21. The oligonucleotide primer for PCR and the sequencing of exon 4, intron 4 and exon 5 of the PTEN/MMAC1 gene and its homologues, characterized by the following sequences:

Zoo43sUV sense
5'- tgtgctgagagacattatgac -3'

SPL5 sense
5'- aaatttaattgcagaggt -3'

Zoo44aRV antisense
5'- ttgtctctggtccttacttc -3'

22. The oligonucleotide primer for PCR and the sequencing of exon 5 of the PTEN/MMAC1 gene and its homologues, characterized by the following sequences:

PTEN se sense
5'- atcttgaccaatggctaagtg -3'

Zoo44aRV antisense
5'- ttgtctctggtccttacttc -3'

23. The oligonucleotide primer for PCR and the sequencing of exon 6 of the PTEN/MMAC1 gene and its homologues, characterized by the following sequences:

PTENex6F sense
5'- gga gta act att ccc agt cag ag -3'

PTENex6R antisense
5'- gca agt tcc gcc act gaa -3'

24. The oligonucleotide primer for PCR and the sequencing of exon 7 of the PTEN/MMAC1 gene and its homologues, characterized by the following sequences:

PTENex7F sense
5'- cct cag ttt gtg gtc tgc ca -3'

PTENex7R antisense
5'- c ctt ttt tag cat ctt gtt ctg ttt -3'

25. The oligonucleotide primer for PCR and the sequencing of exon 8 of the PTEN/MMAC1 gene and its homologues, characterized by the following sequences:

PTENex8F sense
5'- caa aat gtt tca ctt ttg ggt aaa -3'

PTENex8R antisense
5'- taa aat ttg gag aaa agt atc ggt t -3'

26. The oligonucleotide primer for PCR and the sequencing of exon 9 of the PTEN/MMAC1 gene and its homologues, characterized by the following sequences:

PTENex9F sense

5'- gtg aag ctg tac ttc aca aaa ac -3'

PTENex9tga antisense
5'- aaa aaa att cag act ttt gta att tg -3'

27. The method according to claims 1 to 17, characterized in that for the DNA amplification a mixture of oligonucleotides is used which differ at the 3' region of the oligonucleotide as regards its length by one or more nucleotides or which differ as regards their nucleotide sequence at the 3' end of the oligonucleotide at one or more positions.

28. The method according to claims 1 to 17 and 26, wherein the oligonucleotides

sense:
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat -3',
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat t -3',
antisense:
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta c -3',
5'- cag gaa aca gct atg act tgt ctc tgg tcc t -3'

are used for the amplfication.

29. The method according to claims 1 to 17 and 26, wherein the oligonucleotides

sense:
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gaa -3',
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3',

5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gag -3',
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gat -3',
antisense:
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt a -3',
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt g -3',
5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt t -3'

are used for the amplification.

30. The method according to claims 1 to 17, characterized in that DNA sequencing methods are used for the genetic analysis.

31. The method according to claims 1 to 17, characterized in that DNA sequencing techniques are used in the genetic analysis for the PTEN/MMAC1 and/or its pseudogenes and their homologues.

32. The method of distinguishing the DNA of various species, characterized in that at least one hybridization probe pair is used, the melting points of different combinations are determined and compiled for each species into a panel.

33. The method of distinguishing the DNA of various species, characterized in that at least one hybridization probe pair is used and at least one gene segment is amplified, differing hybridization probe pairs hybridize to different gene segments, and the melting points of the different combinations are determined and compiled for each species into a panel and/or compared with this panel for the purpose of identification.

34. The method of distinguishing the DNA of different species according to claim 33, characterized in that at least one hybridization probe pair is used and at least one gene segment of at least one species is amplified, differing hybridization probe pairs hybridize to different gene segments of various species, and the melting points of the different combinations are determined and compiled for each species into a panel and/or compared with this panel for the purpose of identification.

35. The method of distinguishing the DNA of various species according to claims 33 and 34, characterized in that at least two hybridization probes of SEQ Nos. 3 to 8 are used, the melting points of different combinations are determined and compiled for each species into a panel.

36. The method according to claims 33 and 34, characterized in that the species differentiation of pig DNA from various other species is made using the hybridization probe pair A1/A2 as the hybridization probe pair.

37. The method according to claims 33 and 34, characterized in that the hybridization probes are used in combinations C1/C2; A1/B2; A1/A2; C1/A2; B1/B2; B1/A2 for the species differentiation between various species.

38. LightCycler hybridization probes for exon 5, characterized by the sequences:

A1: 5'- tgc ata ttt gtt tca tcc ggg caa att - fluorescein -3'
A2: 5'- LC Red 705 - tta aag gca caa gat ttc tat ggg ga - ph -3'
B1: 5'- tgc ata ttt att aca tcg ggg caa att - fluorescein -3'
B2: 5'- LC Red 640 - aag gca caa gag gcc cta gat ttc ta - ph -3'

C1: 5'- tgc ata ttt gtt aca tcg ggg taa att - fluorescein -3'
C2: 5'- LC Red 640 - aag gca caa gag gcc cta gat ttc ta - ph -3'

39. LightCycler hybridization probes for exon 6, characterized by the sequences

PTENex6FL
5'- tca tct gga tta tag acc agt ggc act - fluorescein -3'

PTENex6LC 640
5'- LC Red 640 - ttc aca aga tga tgt ttg aaa cta ttc caa- ph -3'

PTENex6F*
5'- gtg cca ctg gtc tat aat cca gat- fluorescein -3'

PTENex6L* 705
5'- LC Red 705- ttc ttt aac agg tag cta taa taa tac aca ta- ph -3'

40. The LightCycler hybridization probes for exon 7, characterized by the sequences

PTENex7F*
5'- taa agg tga aga tat att cct cca att ca - fluorescein -3'

PTENex7L*640
5'-LC Red 640- acc cac acg acg gga aga caa g - ph -3'

PTENex7 FL
5'-ggtaacggctgagggaactcaaagtac - fluorescein -3'

PTENex7 LC (705-labeled)
5'-LC Red 705- tgaacttgtcttcccgtcgtgtgg- ph -3'

41. The LightCycler hybridization probes for exon 8, characterized by the following sequences

PTENex8F*
5'- tga caa gga ata tct agt act tac ttt aac aaa-fluorescein -3'

PPTENex8L* 705
5'-LC Red 705 - ctt gac aaa gca aat aaa gac aaa gc- ph -3'

PTENex8 FLU
5'- tgctatcgatttcttgatcacatagacttccatttt - fluorescein -3'

PTENex8 LCR (640-labeled)
5'-LC Red 640- actttttctgaggtttcctctggtcctggtat - ph -3'

42. The LightCycler hybridization probes for exon 9, characterized by the following sequences

PTENex9 FL
5'-aac atc tgg tgt tac aga agt tga act gct- fluorescein -3'

PTENex9 LC 640
5'-LC-640- cct ctg gat ttg acg gct cct cta ct - ph -3'

43. Hybridization probe pair A1/A2: specific to PTEN pseudogene pig, characterized by

SEQ No. 3 A1: 5'- tgc ata ttt gtt tca tcc ggg caa att - fluorescein -3'

SEQ No. 4 A2: 5'-LC Red 705- tta aag gca caa gat ttc tat ggg ga - ph -3'

44. Hybridization probe pair B1/B2: specific to pseudogene man, characterized by

SEQ No. 5 B1: 5'- tgc ata ttt att aca tcg ggg caa att - fluorescein -3'

SEQ No. 6 B2: 5'-LC Red 640- aag gca caa gag gcc cta gat ttc ta -ph -3'

45. Hybridization probe pair C1/C2: specific to PTEN pseudogene man (C2) and homologue of pig (C1), characterized by

SEQ No. 7 - C1: 5'- tgc ata ttt gtt aca tcg ggg taa att - fluorescein -3'

SEQ No. 8 - C2: corresponds to probe B2.

46. DNA sequences and/or fragments of homologues of the PTEN/MMAC1 gene and/or of the homologues of the PTEN/MMAC1 pseudogene, which code for proteins involved in the cell-cell adhesion and cell cycle regulation and have an indispensable function in embryogenesis of the respective species and which are compiled in the annex under "List of species sequences".

47. DNA sequences of homologues of the PTEN/MMAC1 gene and/or of homologues of the PTEN/MMAC1 pseudogene, which are compiled in the annex under "list of species sequences", which as compared to the PTEN/MMAC1 gene and/or the PTEN/MMAC1 pseudogene comprise genetic variants such as base substitutions and/or insertions and/or deletions and are suited for identifying corresponding species.

48. A kit for carrying out the method according to claims 1 to 18 and further claims, comprising:
   a) one or more vessels comprising PCR and/or sequencing oligonucleotides binding to highly conserved genes, the oligonucleotides being optionally labeled radioactively or by means of a

dye or in another way,

b) vessels having further common reagents for DNA amplification and/or DNA analysis, in particular for DNA sequencing,

and

c) a vessel containing a control DNA which is suited for testing the oligonucleotides and the reaction conditions.

49. The kit according to claim 48 for carrying out the method according to claims 1 to 18 and further claims, comprising:

a) one or more vessels with PCR and/or sequencing oligonucleotides according to claims 19 to 26.

50. Kit for identifying species for carrying out the method according to claims 1 to 18 and further claims, comprising:

a) a vessel having an oligonucleotide pair comprising the following sequences:
5'- cga cgt tgt aaa acg acg gcc agt tgt gct gag aga cat tat gac -3' and 5'- cag gaa aca gct atg act tgt ctc tgg tcc tta ctt c -3',

b) two vessels with one of the following sequencing oligonucleotides each, these oligonucleotides being optionally labeled radioactively or by means of a dye or in another way:
5'- cag gaa aca gct atg ac -3' and
5'- cga cgt tgt aaa acg acg gcc agt -3',

c) a vessel containing a control DNA, which is suited for testing the oligonucleotides and the reaction conditions.

51. The kit (Light Cycler Kit) for carrying out the method according to claims 32 to 37 and further claims, comprising

a) one or more vessels containing PCR primers and hybridization probes, which bind to highly conserved genes, the hybridization probes being

optionally labeled by means of a dye,

b) vessels containing further common reagents for DNA amplification and/or DNA analysis, in particular for the Light Cycler Analyses,

and

c) a vessel containing a control DNA which is suited for testing the oligonucleotides and the reaction conditions.

52. The kit (Light Cycler Kit) for carrying out the method according to claims 32 to 37 and further claims, comprising:

a) one or more vessels with PCR primers and hybridization probes according to claims 38 to 42.

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(12) NACH DEM VERTRAG ÜBER DIE INTERNATIONALE ZUSAMMENARBEIT AUF DEM GEBIET DES PATENTWESENS (PCT) VERÖFFENTLICHTE INTERNATIONALE ANMELDUNG

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Veröffentlicht:
— *mit internationalem Recherchenbericht*

[Fortsetzung auf der nächsten Seite]

(54) **Title:** METHOD FOR IDENTIFYING ORGANISMS BY MEANS OF COMPARATIVE GENETIC ANALYSIS AND PRIMERS AND HYBRIDISATION PROBES FOR CARRYING OUT THIS METHOD

(54) **Bezeichnung:** VERFAHREN ZUR IDENTIFIZIERUNG VON ORGANISMEN DURCH VERGLEICHENDE GENETISCHE ANALYSE SOWIE PRIMER UND HYBRIDISATIONSSONDEN ZUR DURCHFÜHRUNG DES VERFAHRENS

(57) **Abstract:** The invention comprises methods, primers and hybridisation probes for identifying organisms by means of comparative genetic analysis and is characterised in that coding and non-coding areas and/or functionally significant areas of highly conserved genes, pseudogenes or homologues are amplified using the PCR and then genotyped and analysed. The comparison of coding and non-coding areas of highly conserved genes, pseudogenes or homologues ensures that a single oligonucleotide pair bonds to DNA sequences that are highly conserved between different species, hereby allowing the amplification of a gene segment that is identical for all of the species. The oligonucleotides include one or more gene areas with the greatest possible sequence differences between different species. The determination of the gene sequence of this highly polymorphous area in a subsequent reaction step enables the gene sequence to be allocated to a specific species. In particularly preferred variants of embodiments of the invention, oligonucleotide pairs are found that make it possible to amplify the highly conserved tumour suppresser gene PTEN/MMAC1, its pseudogene and their homologues.

(57) **Zusammenfassung:** Die Erfindung umfaßt Verfahren, Primer und Hybridisationssonden zur Identifizierung von Organismen durch vergleichende genetische Analyse, dadurch gekennzeichnet, daß man kodierende, nichtkodierende Bereiche und/oder funktionell bedeutende Bereiche von hochkonservierten Genen, Pseudogenen oder Homologen mit Hilfe der PCR amplifiziert und nachfolgend genotypisiert und analysiert. Der Vergleich von kodierenden und nicht kodierenden Bereichen von hochkonservierten Genen, Pseudogenen oder Homologen gewährleistet, daß ein einziges Oligonukleotidpaar an DNA-Sequenzen, die zwischen verschiedenen Spezies hochgradig konserviert sind, bindet und damit die Amplifikation eines für alle Spezies identischen Genabschnitts erlaubt. Die Oligonukleotide schließen einen oder mehrere Genbereiche ein, die zwischen verschiedenen Spezies möglichst große Sequenzunterschiede aufweisen. Die Bestimmung der Gensequenz dieses hochgradig polymorphen Bereichs in einem darauf folgenden Reaktionsschritt erlaubt es, die Gensequenz einer spezifischen Spezies zuzuordnen. In besonders bevorzugten Ausführungsvarianten der Erfindung wurden Oligonukleotidpaare gefunden, die die Amplifikation des hochkonservierten Tumorsuppressorgens PTEN/MMAC1, seines Pseudogens und ihrer Homologen ermöglicht.

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Figure 1:

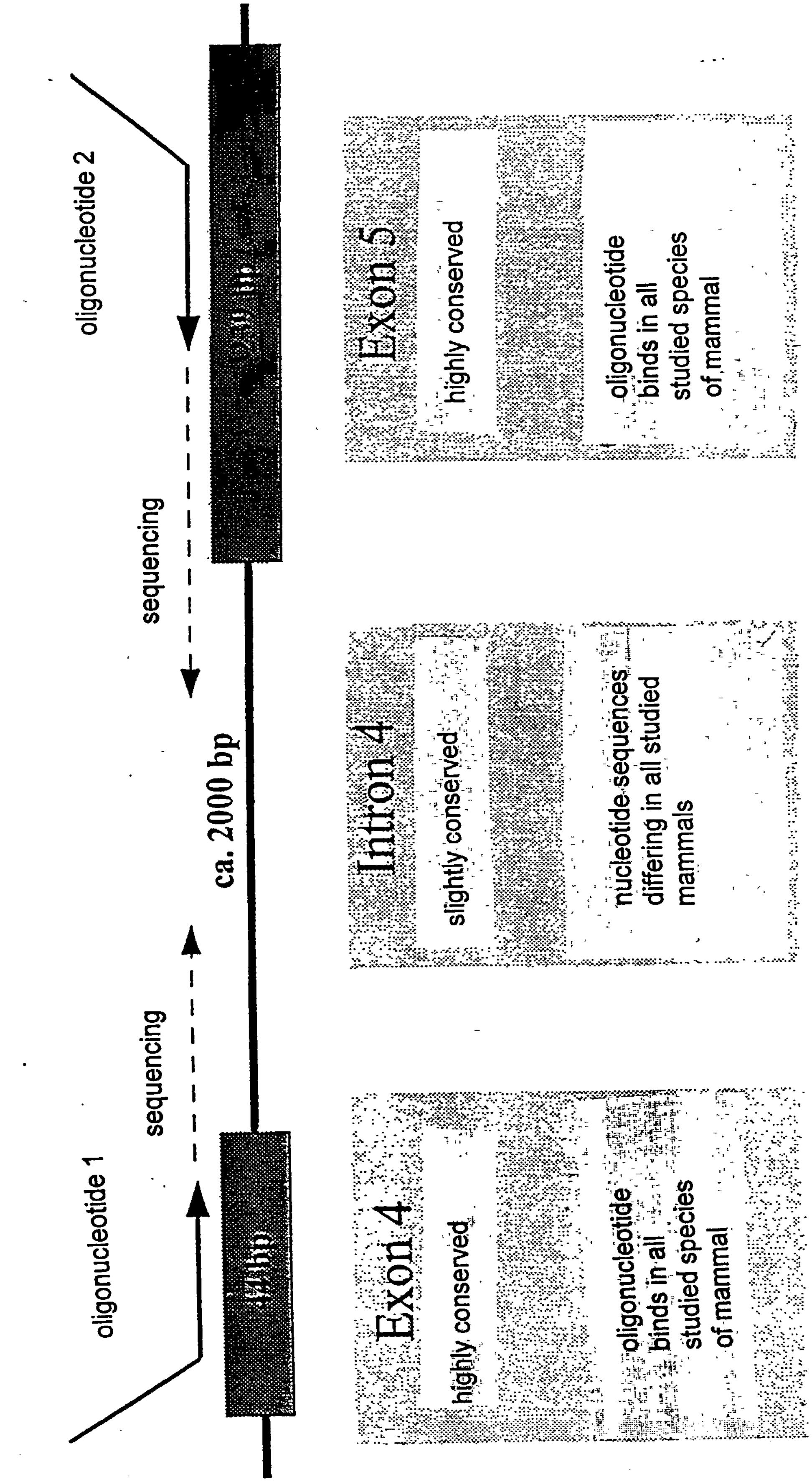

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Figure 2

```
                          10        20        30        40        50        60        70
man               ...T..C..T...A......--.-.....C...A....CTCT...A.CC..-.G-.-..C.-......
African elephant  ...C..A..C...C......TC..G.....A...T....TAAG...G.TT..C.TA.C..T.A......

                          80        90        100       110       120       130       140
man               T.......-.-.....G.A.....CA.....-..............G.................--....TT
African elephant  C.......T.T.....A.G.....TG.....G..............-................GG....A-

                          150       160       170       180       190       200       210
man               .................G.........................A.................T........
African elephant  .................T.........................G.................C........

                          220       230       240       250       260       270       280
man               .........A............................................................
African elephant  .........G............................................................

                          290       300       310       320       330       340       350
man               ......................................................A..........A.........
African elephant  ......................................................T..........G.........
```

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Figure 3

```
                      10        20        30        40        50        60        70
pig          ....C......C..............G..............T.....T...............T......
pig liver    ....C......C..............G..............T.....T...............T......
beef salami  ....A......T..............A..............C.....C...............C......

                      80        90       100       110       120       130       140
pig          ....T.................................................................
pig liver    ....T.................................................................
beef salami  ....C.................................................................

                     150       160       170       180       190       200       210
pig          .C.......A...T................T............G..T....C...................
pig liver    .C.......A...T................T............G..T....C...................
beef salami  .G.......G...C................A............A..A....G...................

                     220       230
pig          .....---------...........
pig liver    .....---------...........
beef salami  .....GGCCCTAGA...........
```

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Figure 4: **Positions of the hybridization probes in exon 5 of the PTEN gene, pseudogene and their homologues**

	150	B1		B2	220
man pseudogene	ATATG	**TGCATATTTATTACATCGGGGCAAATT**	TTTA	**AAGGCACAAGAGGCCCTAGATTTCTA**	TGGGGAAGT
		C1		C2	
pig gene	ATTTG	**TGCATATTTGTTACATCGGGGTAAATT**	TTTA	**AAGGCACAAGAGGCCCTAGATTTCTA**	TGGGGAAGT
		A1		A2	
pig pseudogene	ATTTG	**TGCATATTTGTTTCATCCGGGCAAATT**	T	**TTAAAGGCACAAGA ---- --- -- TTTCTATGGGGA**	AGT

Figure 5: Melting point panel

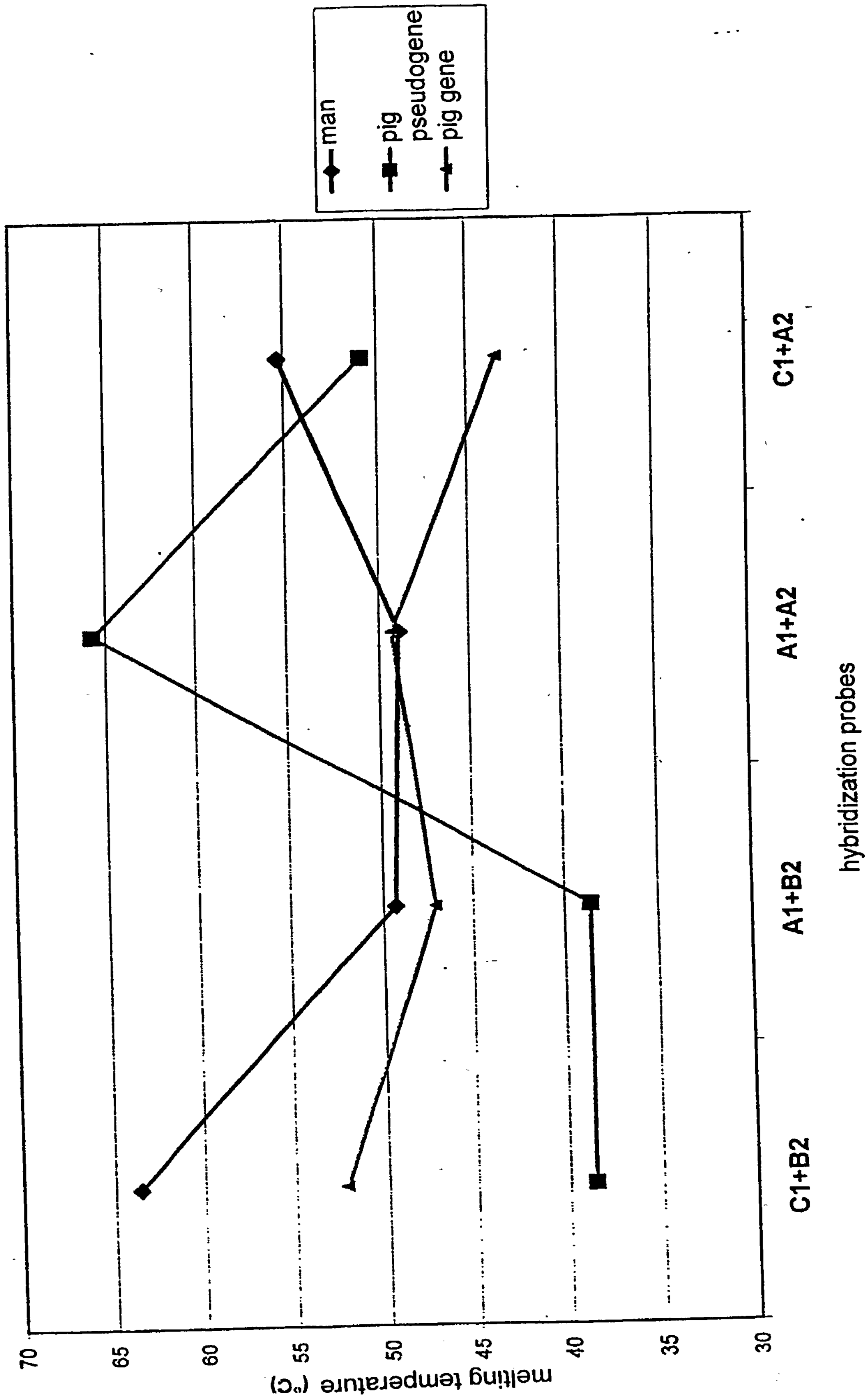


Figure 6: Melting point with probe A1 + A 2

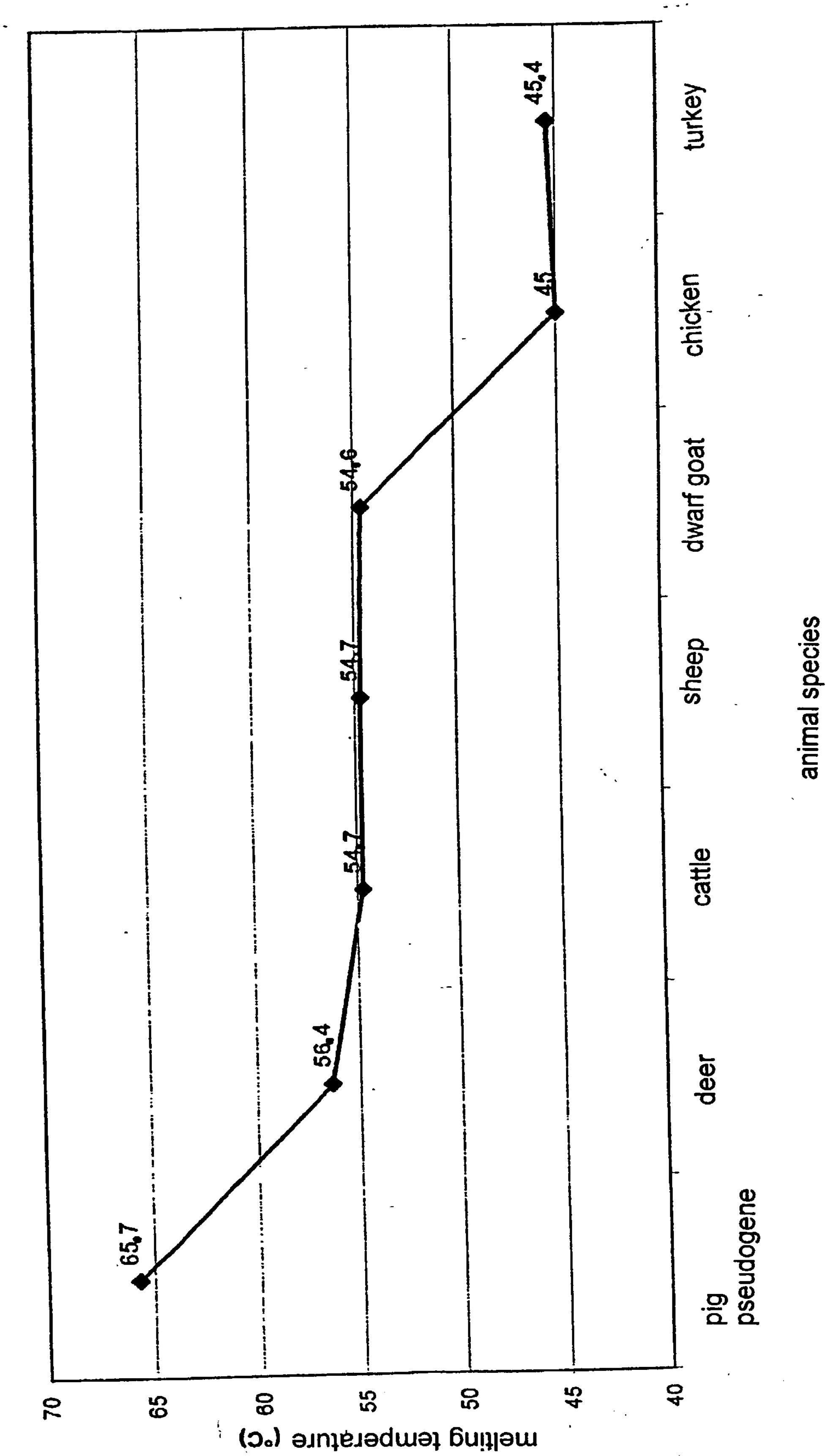


Figure 7: Melting point panel

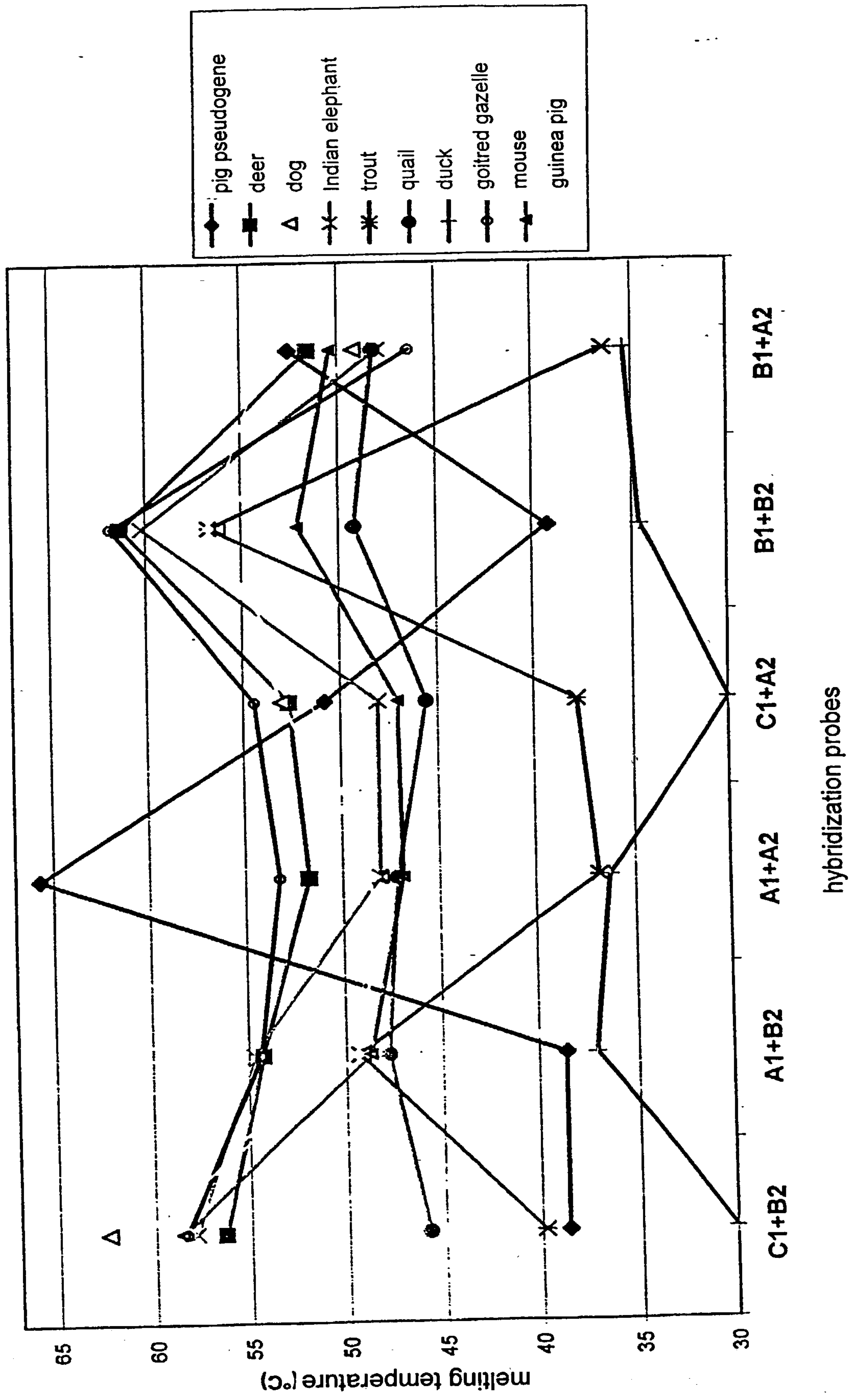
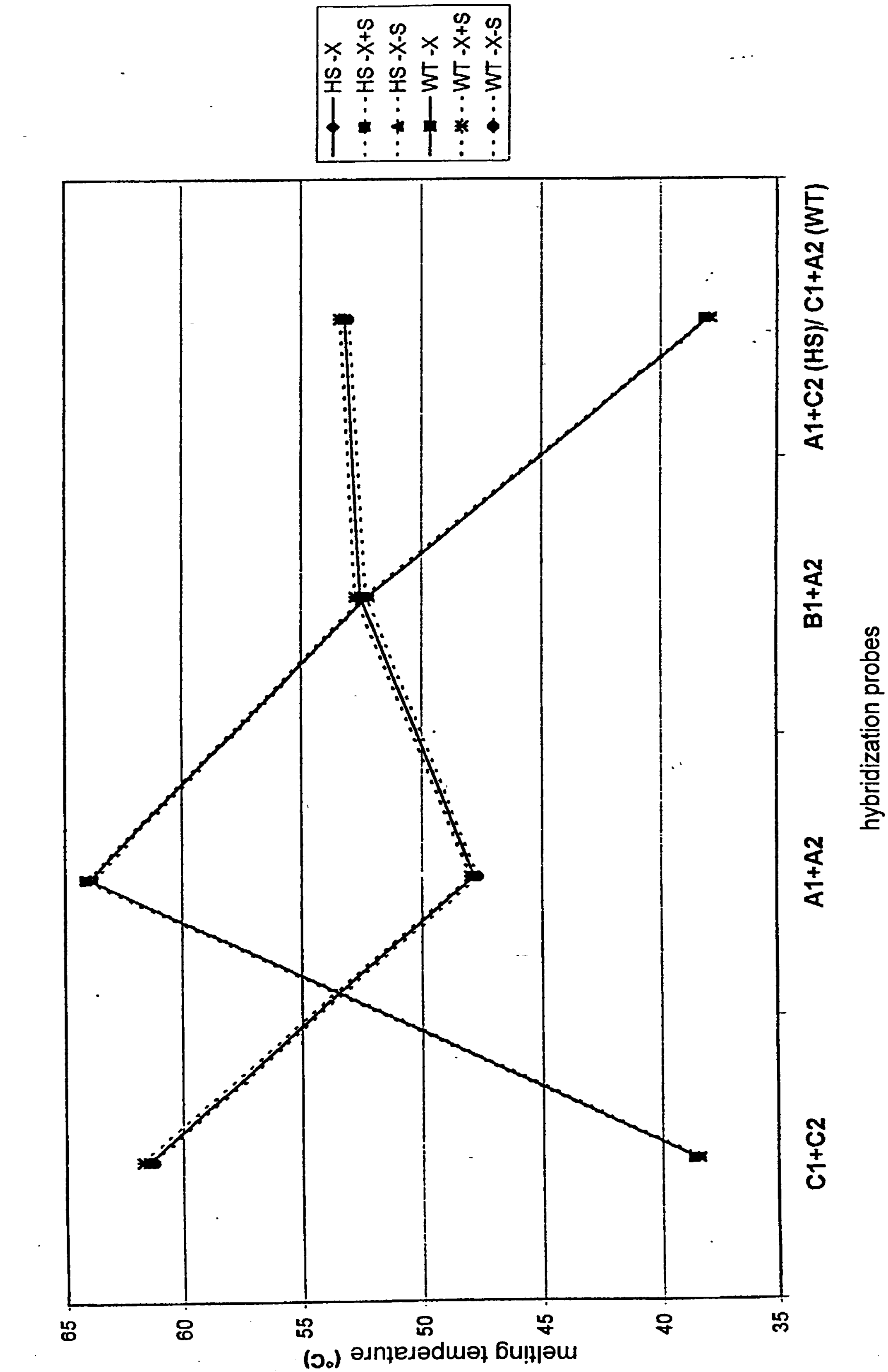


Figure 8: Standard deviations of select probes



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10 Rec'd PCT/PTO 19 FEB 2002

Patent
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of Hans Konrad SCHACKERT *et al.*	Group Art Unit: Unassigned
Serial No.: 09/936,738 Corresponding to PCT/EP00/02330	Examiner: Unassigned
International Filing Date: 3 March 2000	**ATTENTION: BOX SEQUENCE**
For: METHOD FOR IDENTIFYING ORGANISMS BY MEANS OF COMPARATIVE GENETIC ANALYSIS AND PRIMERS AND HYBRIDISATION PROBES FOR CARRYING OUT THIS METHOD	

DECLARATION PURSUANT TO 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

I, Deborah H. Yellin, declare as follows:

1. That the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same in compliance with § 1.821(f).

2. That the submission, filed in accordance with 37 C.F.R. § 1.821(g)[or (h)], herein does not include new matter [or go beyond the disclosure in the international application].

Serial No.: 09/936,738

I hereby declare that all statements made herein of my own knowledge are true and that all statements were made on information and belief and are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

February 22, 2002
Date

Deborah H. Yellin
Registration No. 30,427

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S 1048 US

COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY (Includes Reference to Provisional and PCT International Applications)	Attorney's Docket No. 012627-025

As a below named inventor, I hereby declare that:
My residence, post office address and citizenship are as stated below next to my name;
I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

METHOD FOR IDENTIFYING ORGANISMS BY MEANS OF COMPARATIVE GENETIC ANALYSIS AND PRIMERS AND HYBRIDIZATION PROBES FOR CARRYING OUT THIS METHOD

the specification of which (check only one item below):

☐ is attached hereto.

☐ was filed as United States application
Number ______
on ______
and was amended
on ______ (if applicable).

☒ was filed as PCT international application
Number PCT/EP00/02330
on 16 March 2000
and was amended
on ______ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, §119 (a)-(e) of any foreign application(s) for patent or inventor's certificate or of any PCT international application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application(s) for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 U.S.C. §119:

COUNTRY (if PCT, indicate "PCT")	APPLICATION NUMBER	DATE OF FILING (day, month, year)	PRIORITY CLAIMED UNDER 35 U.S.C. §119
Germany	199 11 656.3	16-03-99	X Yes _ No
Germany	199 64 112.9	31-12-99	X Yes _ No
			_ Yes _ No
			_ Yes _ No
			_ Yes _ No

I hereby claim the benefit under Title 35, United States Code § 119(e) of any United States provisional application(s) listed below.

______ (Application Number) ______ (Filing Date)

______ (Application Number) ______ (Filing Date)

(05/01)

COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY (CONT'D) (Includes Reference to Provisional and PCT International Applications)	Attorney's Docket No. 012627-025

I hereby claim the benefit under Title 35, United States Code, §120 of any United States applications(s) or PCT international application(s) designating the United States of America that is/are listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in that/those prior application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to the patentability as defined in Title 37, Code of Federal Regulations §1.56, which became available between the filing date of the prior application(s) and the national or PCT international filing date of this application:

PRIOR U.S. APPLICATIONS OR PCT INTERNATIONAL APPLICATIONS DESIGNATING THE U.S. FOR BENEFIT UNDER 35 U.S.C. §120:

U.S. APPLICATIONS		STATUS *(check one)*		
U.S. APPLICATION NUMBER	U.S. FILING DATE	PATENTED	PENDING	ABANDONED

PCT APPLICATIONS DESIGNATING THE U.S.			STATUS		
PCT APPLICATION NO.	PCT FILING DATE	U.S. APPLICATION NUMBERS ASSIGNED (if any)	PATENTED	PENDING	ABANDONED

I hereby appoint the following attorneys and agent(s) to prosecute said application and to transact all business in the Patent and Trademark Office connected therewith and to file, prosecute and to transact all business in connection with international applications directed to said invention:

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Robert S. Swecker	19,885	James W. Peterson	26,057	Todd R. Walters	34,040
Platon N. Mandros	22,124	Teresa Stanek Rea	30,427	Ronni S. Jillions	31,979
Benton S. Duffett, Jr.	22,030	Robert E. Krebs	25,885	Harold R. Brown III	36,341
Norman H. Stepno	22,716	William C. Rowland	30,888	Allen R. Baum	36,086
Ronald L. Grudziecki	24,970	T. Gene Dillahunty	25,423	Brian P. O'Shaughnessy	32,747
Frederick G. Michaud, Jr.	26,003	Patrick C. Keane	32,858	Kenneth B. Leffler	36,075
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Samuel C. Miller, III	27,360	Peter K. Skiff	31,917	Mary Ann Dillahunty	34,576
Robert G. Mukai	28,531	Richard J. McGrath	29,195		
George A. Hovanec, Jr.	28,223	Matthew L. Schneider	32,814		
James A. LaBarre	28,632	Michael G. Savage	32,596		
E. Joseph Gess	28,510	Gerald F. Swiss	30.113		
R. Danny Huntington	27,903	Charles F. Wieland III	33,096		

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY (CONT'D) (Includes Reference to Provisional and PCT International Applications)	Attorney's Docket No. 012627-025

1-00

FULL NAME OF SOLE OR FIRST INVENTOR	SIGNATURE	DATE
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2-00

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RESIDENCE: Jahnstraße 14, D-68526 Ladenburg, Germany DEX		CITIZENSHIP: German
POST OFFICE ADDRESS: Jahnstraße 14, D-68526 Ladenburg, Germany		

3-00

FULL NAME OF THIRD JOINT INVENTOR, IF ANY	SIGNATURE	DATE
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POST OFFICE ADDRESS: Senefelder Straße 2/Zi. 620, D-01307 Dresden, Germany		

4-00

FULL NAME OF FOURTH JOINT INVENTOR, IF ANY	SIGNATURE	DATE
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RESIDENCE: Weinbergstraße 50, D-01129 Dresden, Germany DEX		CITIZENSHIP: German
POST OFFICE ADDRESS: Weinbergstraße 50, D-01129 Dresden, Germany		

FULL NAME OF FIFTH JOINT INVENTOR, IF ANY	SIGNATURE	DATE
RESIDENCE		CITIZENSHIP
POST OFFICE ADDRESS		

FULL NAME OF SIXTH JOINT INVENTOR, IF ANY	SIGNATURE	DATE
RESIDENCE		CITIZENSHIP
POST OFFICE ADDRESS		

FULL NAME OF SEVENTH JOINT INVENTOR, IF ANY	SIGNATURE	DATE
RESIDENCE		CITIZENSHIP
POST OFFICE ADDRESS		

FULL NAME OF EIGHTH JOINT INVENTOR, IF ANY	SIGNATURE	DATE
RESIDENCE		CITIZENSHIP
POST OFFICE ADDRESS		

09/936738

10 Rec'd PCT/PTO 19 FEB 2002

SEQUENCE LISTING

<110> Schackert, Hans Konrad
      Hahn, Matthias

<120> Method for Identifying Organisms by Means of Comparative Genetic
      Analysis and Primers and Hybridisation Probes for Carrying Out
      This Method

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<140> US 09/936,738
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<400> 63
aggtcaagtc taagtcgaat c 21

<210> 64
<211> 67
<212> DNA
<213> Man

<400> 64
cagccatcat caaagagatc gttagcagaa acaaaaggag atatcaagag gatggattcg 60
acttaga 67

<210> 65
<211> 68
<212> DNA
<213> Chimpanzee

<400> 65
acagccatca tcaaagagat cgttagcaga aacaaaagga gatatcaaga ggatggattc 60
gacttaga 68

<210> 66
<211> 64
<212> DNA
<213> Pig

<400> 66
ccatcatcaa agagatcgtt agcagaaaca aaaggagata tcaagagaat ggattcgact 60
taga 64

<210> 67
<211> 64
<212> DNA
<213> Wild boar

<400> 67
ccatcatcaa agagatcgtt agcagaaaca aaaggagata tcaagagaat ggattcgact 60
taga 64

<210> 68

<211> 67
<212> DNA
<213> Cattle

<400> 68
cagccatcat caaagagatc gttagcagaa acaaaaggag atatcaagag gatggattcg 60
acttaga 67

<210> 69
<211> 67
<212> DNA
<213> Sheep

<400> 69
cagccatcat caaagagatc gttagcagaa acaaaaggag atatcaagag gatggattcg 60
acttaga 67

<210> 70
<211> 67
<212> DNA
<213> Goat

<400> 70
agccatcatc aaagagatcg ttagcagaaa caaaaggaga tatcaagagg atggattcga 60
cttagac 67

<210> 71
<211> 68
<212> DNA
<213> Red buffalo

<400> 71
acagccatca tcaaagagat cgttagcaga aacaaaagga gatatcaaga ggatggattc 60
gacttaga 68

<210> 72
<211> 67
<212> DNA
<213> Deer

<400> 72
cagccatcat caaagagatc gttagcagaa acaaaaggag atatcaagag gatggattcg 60
acttaga 67

<210> 73
<211> 66
<212> DNA
<213> Roe deer

<400> 73
agccatcatc aaagagatcg ttagcagaaa caaaaggaga tatcaagagg atggattcga 60
cttaga 66

<210> 74
<211> 67
<212> DNA
<213> Goitred gazelle

<400> 74
cagccatcat caaagagatc gttagcagaa acaaaaggag atatcaagag gatggattcg 60
acttaga 67

<210> 75
<211> 68
<212> DNA
<213> Horse

<400> 75
acagccatca tcaaagagat cgttagcaga aacaaaagga gatatcaaga ggatggattc 60
gacttaga 68

<210> 76
<211> 58
<212> DNA
<213> Dog

<400> 76
gccatcatca aagagatcgt cagcagaaac aaaaggcgct accaggagga tggattcg 58

<210> 77
<211> 67
<212> DNA
<213> Sun bear

<400> 77
agccatcatc aaagagatcg ttagcagaaa caaaaggaga tatcaagagg atggattcga 60
cttagac 67

<210> 78
<211> 69
<212> DNA
<213> Rabbit

<400> 78
acagccatca tcaaagagat cgttagcaga aacaaaagga gatatcaaga ggatggattc 60
gacttagac 69

<210> 79
<211> 65
<212> DNA
<213> Hare

<400> 79
cagccatcat caaagagatc gttagcagaa acaaaaggag atatcaagag gatggattcg 60
actta 65

<210> 80
<211> 59
<212> DNA
<213> Antelope

<400> 80
ccatcatcaa agagatcgtt agcagaaaca aaaggagata tcaagaggat ggattcgac 59

<210> 81

<211> 65
<212> DNA
<213> Kangaroo

<400> 81
gccatcatca aagagatcgt gagcagaaac aaaaggagat accaagagga tggattcgac 60
ttaga 65

<210> 82
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENex2F sense

<400> 82
atatttatcc aaacattatt gctat 25

<210> 83
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENex2R antisense

<400> 83
cttactacat catcaatatt gttcc 25

<210> 84
<211> 69
<212> DNA
<213> Man

<400> 84
tccaaacatt attgctatgg gatttcctgc agaaagactt gaaggcgtat acaggaacaa 60
tattgatga 69

<210> 85
<211> 69
<212> DNA
<213> Chimpanzee

<220>
<221> misc_feature
<222> (1)...(69)
<223> n = A,T,C or G

<400> 85
aaacattatt gctatgggat ttcctgcaga aagacttgaa ggcgtatana ggaacaatat 60
tgatgatgt 69

<210> 86
<211> 70
<212> DNA
<213> Domestic pig

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<400> 86
ccaaacatta ttgctatggg gtttcctgca gaaagacttg aaggcgtata caggaacaat 60
attgatgatg                                                        70

<210> 87
<211> 71
<212> DNA
<213> Wild boar

<400> 87
aaacattatt gctatggggt ttcctgcaga aagacttgaa ggcgtataca ggaacaatat 60
tgatgatgta g                                                      71

<210> 88
<211> 63
<212> DNA
<213> Cattle

<400> 88
cattattgct atgggctttc ctgcagaaag acttgaaggt gtatacagga acaatattga 60
tga                                                               63

<210> 89
<211> 62
<212> DNA
<213> Sheep

<400> 89
ttattgctat ggggtttcct gcagaaagac ttgaaggcgt gtacaggaac aatattgatg 60
at                                                                62

<210> 90
<211> 58
<212> DNA
<213> Goat

<400> 90
ttattgctat ggggtttcct gcagaaagac ttgaaggcgt gtacaggaac aatattga   58

<210> 91
<211> 64
<212> DNA
<213> Red buffalo

<220>
<221> misc_feature
<222> (1)...(64)
<223> n = A,T,C or G

<400> 91
cattattgct atggggtttc ctgcagaaag acttgaaggc gtatnnagga acaatattga 60
tgat                                                              64

<210> 92
<211> 68
<212> DNA
<213> Deer
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<400> 92
tttatccaaa cattattgct atggggtttc ctgcagaaag acttgaaggc gtatacagga 60
acaatatt 68

<210> 93
<211> 58
<212> DNA
<213> Roe deer

<220>
<221> misc_feature
<222> (1)...(58)
<223> n = A,T,C or G

<400> 93
ttattgctat ggggtttcct gcagaaagac ttgaaggcgt atannggaac aatattga 58

<210> 94
<211> 65
<212> DNA
<213> Goitred gazelle

<400> 94
ccaaacatta ttgctatggg gtttcctgca gaaagacttg aaggcgtata caggaacaat 60
attga 65

<210> 95
<211> 64
<212> DNA
<213> Horse

<400> 95
attattgcta tggggtttcc tgcagaaaga cttgaaggcg tatacaggaa caatattgat 60
gatg 64

<210> 96
<211> 67
<212> DNA
<213> Dog

<220>
<221> misc_feature
<222> (1)...(67)
<223> n = A,T,C or G

<400> 96
ttccaaacat tattgctatn gggtttcctg cagaaagact tgaaggcgta tacnggaaca 60
atattga 67

<210> 97
<211> 65
<212> DNA
<213> Sun bear

<220>
<221> misc_feature
<222> (1)...(65)

<223> n = A,T,C or G

<400> 97
tccaaacatt attgctatng ggtttcctgc agaaagactt gaaggcgtat acaggaacaa 60
tattg 65

<210> 98
<211> 62
<212> DNA
<213> Rabbit

<400> 98
gctatgggat ttcctgcaga aagacttgaa ggcgtataca ggaacaatat tgatgatgta 60
gt 62

<210> 99
<211> 59
<212> DNA
<213> Hare

<400> 99
acattattgc tatgggattt cctgcagaaa gacttgaagg cgtatacagg aacaatatt 59

<210> 100
<211> 48
<212> DNA
<213> Antelope

<400> 100
ttgctatggg gtttcctgca gaaagacttg aaggcgtata caggaaca 48

<210> 101
<211> 77
<212> DNA
<213> Turkey

<400> 101
tttatccaaa cattattgct atgggttttc ctgcggagag gcttgaagga gtataccgga 60
acaatattga tgatgta 77

<210> 102
<211> 73
<212> DNA
<213> Chicken

<400> 102
atttatccaa acattattgc tatgggtttt cctgcggaga ggcttgaagg agtataccgg 60
aacaatattg atg 73

<210> 103
<211> 61
<212> DNA
<213> Duck

<400> 103
ttattgctat gggttttcct gcagagaggc ttgaaggagt gtaccggaac aatattgatg 60
a 61

09936738 .091701

<210> 104
<211> 62
<212> DNA
<213> Quail

<400> 104
cattattgct atgggttttc ctgcggagag gcttgaagga gtataccgga acaatattga 60
tg 62

<210> 105
<211> 73
<212> DNA
<213> Goose

<400> 105
tttatccaaa cattattgct atgggttttc ctgcagagag gcttgaagga gtgtaccgga 60
acaatattga tga 73

<210> 106
<211> 66
<212> DNA
<213> Ostrich

<400> 106
ccaaacatta ttgctatggg ttttccggcg gagaggcttg aaggagtgta ccggaacaat 60
attgat 66

<210> 107
<211> 59
<212> DNA
<213> Pigeon

<400> 107
cattattgct atgggttttc ctgcggagag gcttgaagga gtataccgga acaatattg 59

<210> 108
<211> 60
<212> DNA
<213> Varan

<400> 108
cattattgct atgggttttc ctgcggagag gcttgaagga gtataccgga acaatattga 60

<210> 109
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Zoo43sUV

<400> 109
tgtgctgaga gacattatga c 21

<210> 110
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Zoo44aRV

<400> 110
ttgtctctgg tccttacttc 20

<210> 111
<211> 654
<212> DNA
<213> Man

<400> 111
ttatgacacc gccaaattta attgcagagt atgaatgtac tgtactatgt tgtataactt 60
aaacccgata gactgtatct tactgtcata acaataatga gtcatccaga ttatcgagtg 120
agatacatat ttaagaatta tctttaaaaa tttcaaaaat tttaatttta ctgttgtgtt 180
ttaggaaaaa gtattgcata aagctattaa tattgtcagg aagactaaag tgcagcatag 240
actaagaatt aggaaaattc ctagactaaa aatagtataa ggagagggtt tacctactat 300
ttgaggcagt tggtctaata gtaagcaatc acagggagaa agcagaacta cttaactctt 360
ctgtgttgag gaatgacata aaaggtagga aaggatataa caaatgttga taagaggagt 420
ctgatggatg agaggaggga actgctttaa atgagtttct acttcagaca taagttaatt 480
ctcagagccc acaaaaactt tcacttttat ttgtgaaata caactcagtt ctcatggctt 540
aacactttaa accatgagaa aactgaagag ttgagagctt ggcagatgct gctgtgatag 600
tcaaaagaaa gtgggtgcat gagctactat tgatgtattt gccatggtcc ctcc 654

<210> 112
<211> 582
<212> DNA
<213> Dog

<400> 112
atgtaataaa tatgcacaaa tcattacacc agttcgtccc tttccagctt tacagtgaat 60
tgctgcaaca tgattgtcat cttcacttag ccattggtca agatcttcac aaaagggttt 120
gataagttct agctgtggtg gattatggtc ttcaaaagga tactgtgcaa ctgtggtaaa 180
aagataacct cagaattaga aaaaagtctt tcctgaactg tttattaaaa gtaggttaac 240
tttagaaaca ttgcatgtaa gcttaacaga tgtttaaaag aaaaacggaa ctccagagaa 300
aaataatttg ctgtctgata attttccaat ttttgaatag aaaatagtct ctcattaatt 360
cttaaaccta ccactadgag agagaggcta agcattattt tcccccactt taatgaaaga 420
ggaaactttg caatggagag ggagcacacg tcaacatatc agagggaaga ggcaaactca 480
aaatgaaatg gcacacaggt ttcctgtcag ggctctcaat gcattttctg acaaaaggag 540
tcataatatt tataatacta cgtcatccaa aatatatatt cc 582

<210> 113
<211> 376
<212> DNA
<213> Cattle

<220>
<221> misc_feature
<222> (1)...(376)
<223> n = A,T,C or G

<400> 113
taggtacaca tattgtgtta gataacttga agccaacagt ctaaatttta ctgtcatacc 60
aataatgaat aatctcaagt attaagtgat atatttatct taaagatggt ctgagaaaat 120

ttgaaattaa ttttgctgtt gtgtttttgg aaataagtat catgtaaatg aggaagacta 180
aattgaatta actgaaaact aggagaaatt tatagactaa cagaataaat agagggttat 240
atctgtgatt tgaggcattt ggcatgatag taagagatta caggggagaa aggagaatgg 300
cttaattctg taatggaaca tgacctgtac agtgggaaaa ggggtataat gaantatgga 360
tnaaaaggag cctgaa 376

<210> 114
<211> 673
<212> DNA
<213> Mouse

<400> 114
ttatgacacc gccaaattta actgcagagg tatgtataaa cataaccaca gcatactgta 60
taactaaaga ccaatagact tgtcttttac tgcctggtga taattatcaa gattagtgag 120
ataaaaatct taagaatggc ctttgacaat taaaaaaagt gtatttaatg ttagagttgt 180
tctttaagac ctatctattg tcaggaaaac taaatcacag aatacttgga gaggtcccaa 240
gactaaacta ggattggagg tgcttattga cggtgtggga cagctagcgc tgctggaaac 300
aatcacaaga agagagcaga accattttaa cttttctaca tcgaagaatg gcataaagtt 360
aggaaaagat gtagcatcgg tctgtctgtc tgtctgtctg cctgtctgtc ttctcagaat 420
catgaagcac taaggagtaa gtaagaacag tttctggggg accgacagac ctaggctact 480
gctcattagg aaacatgcca tggttgaagg tcacttagct ttaaatgtac attttaacag 540
actcttgaat gttcttgtgt gccactgggg gaaatgaggt cgggagcaca gttagacaga 600
tggttaagta aaagctggcc tgcagcctct tggtgaatgt agtttgccat tgtttaccac 660
agagctttcc tgt 673

<210> 115
<211> 411
<212> DNA
<213> Horse

<400> 115
aatgtacagt attttgttat ataactgaaa accagtagac taagtcttac tgtcacagca 60
gtaatgaata ctcttgatta ttaagtgaga taaatattta tcttaaaaag ataatcttag 120
aaaatttgaa aaataaattt aactttgctg ttgtatttta gaaaacaagt atcatataaa 180
ccaactggta gtattaggaa gactaaattg aagaatagac taagaattag gatgtaatag 240
taagagattg catggagaaa gcagaacgac ttaactctgg caaggagcgt gacctaaaag 300
gtggaaaagg gtataacaga tgtggataca aggagcctga acagatgaga gcagggaact 360
gcttcaaatg agttcttttc caagtatagt aaattgtttc tcagagccca c 411

<210> 116
<211> 566
<212> DNA
<213> Sheep

<220>
<221> misc_feature
<222> (1)...(566)
<223> n = A,T,C or G

<400> 116
aaaaatttgc nnnngatgta acaaatatgc acaaatcatt acaccagttc gtccctttcc 60
agctttacag tgaattgctg caacatgatt gtcatcttca cttagccatt ggtcaagatc 120
ttcacaaaag ggtttgataa gttctaactg ttggtggatt atggtcttca aagggatact 180
gtgcaactgt gataaaaaga taaccgcaga tatatgaaaa taatctcact tgaattgctt 240
attacaagta ggctaacttt agaaatgttg catacaaata gtttaaaaat gtctgaacta 300
tagaggaaaa gaatttattg tctgataatt ttctaatttt cgaacagaaa ataatctctc 360
attaactcaa atttatccat tcgacaggta agacaagtat tatttcctca ctctatgatg 420

gaggcaatgg aggagcaaca tatcagaggt cacaacataa cggaggaaga ggcaaactca 480
gaatgaaacg tcgcacgagc ctcttagcag ggctctcaat acgttcctag caaaagggac 540
tggtaacatc tataatatcg cattat 566

<210> 117
<211> 497
<212> DNA
<213> Turkey

<400> 117
aagctgcatt ttgccaggtg taaggaactg acagagacaa ccaagaccaa agcatttcag 60
gctgaattcc cctckttcct cccacctcct ctgaacaaat ggaggttctg acagagtgga 120
gagattaatt cagaatatgt gtgcacagta cacctggcag accccacaaa gcttggctca 180
aagaacaaag atgaaacaaa ggcatgaata gagcagtaga aggatttaca aaaggacaaa 240
agatgggcag ccatttaaag gtgacagtaa tttcttaagt aaatgtcaaa actcttcaaa 300
gaagcaaggg ggataatatt catgaatact taaggctgaa acgtgaacat gttgatttgc 360
catttggaag gttatgtttc cttcttatct cctctctgat agcttcaata atgggcacta 420
aaattcgttc ctgaaaaaat gcaaagaaat cactcagtgt ctgaggacgt gttgatttca 480
catgtattga aatcagt 497

<210> 118
<211> 365
<212> DNA
<213> Trout

<220>
<221> misc_feature
<222> (1)...(365)
<223> n = A,T,C or G

<400> 118
cattatgacn nnnnnnnatt caattgcaga ggattagata ttacatcaga gtgaaaccat 60
tatcactgtc tttcaggcag tcagtgaatg aatcaatctt tcactaaaaa cccacgtgtg 120
acgctaacta actgagcccg gtctctgtct gtctctctcc agttgcacaa tatccgtttg 180
aggatcacaa tccgccccag ctggagctga tcaaaccgtt ctgcgaagat cttggccttt 240
ggttaagtga agacgacaat catgtggcgg cgattcactk taaarctgga aaggacgtac 300
gggtgtcatg atctgtgctt acctgttaca ccggggcaag ttcctcaaag cacaagaagc 360
tctcg 365

<210> 119
<211> 656
<212> DNA
<213> Roe deer

<400> 119
gtataggtac acttactatg ttagataact tgaggccaac agtctaaatt ttactatcat 60
accagtaatg aataatctca agtattaagt gatacagtca tcttaaagat gatcttagaa 120
aatttgaaat taattttgct gttgtgtttt tggaaacaag tgtcatgtaa atgagggaga 180
ctaaactgaa ttaactgaaa actaggagaa atttatagac tgacagaata aagaaagggt 240
tatatctgtg atttgaggca tttggcgtaa tagtaagaga ttacagggag aaaggagaat 300
gatttaattc tataatggaa catgacctgc acagtggaaa aagggtataa tgaaatataa 360
awaaaaggag cctgatagat gagagcaaga actgctttaa gtgaattttt ctccaggtat 420
agtatatttt atctcagagt ccacaaatac tttcatttgt ttttgtggaa ctcttagaac 480
gacgagagac caggaacatt gagaagctaa tatatttgcc attgttcctt cctaaatatt 540
tagcacaggc tttcaaacag ttggtttaag aattcagaag tgctaataac tgagagcaag 600
ggtagattta ttactaagaa tgtttcattt ttggtggatt ttgctatttc tggtca 656

<210> 120
<211> 405
<212> DNA
<213> Deer

<220>
<221> misc_feature
<222> (1)...(405)
<223> n = A,T,C or G

<400> 120
gtataggtac actttnnaag ccaacagtct aaattttact gtcataccaa taatgaataa 60
tctcaagtat taagtgatat atttatctta aagatgatct tagaaaattt gaaactaatt 120
ttgctgttgt gtttttggaa acaagtgtca tgtaaatgag ggagaccata actgaattaa 180
ctgaaaactg ggaaaaattt atagactaac agaataaaga aagggttata tctgtggttt 240
gaggcgtttg acgtaatagt aagagattac agggagaaag gagaatgact taattctata 300
atggaacacg acctgcacag tggaaaaagg gtataatkaa atgtagataa aggagcctga 360
tagttgagag caagaactgc tttaagtgag tttttctcca ggtgt 405

<210> 121
<211> 522
<212> DNA
<213> Chimpanzee

<220>
<221> misc_feature
<222> (1)...(522)
<223> n = A,T,C or G

<400> 121
cattatgacn nnnnnnnnnn nnattgcaga ggtaggtatg aatgtactgt actatgttgt 60
ataacttaaa cccgatagac tgtatcttac tgtcataaca ataatgagtc atctagatta 120
tcgagtgaga tacatattta tcttaagaat tatctttaaa aatttcaaaa attttaattt 180
tactcttgtg ttttaggaaa aaagtattgc ataaagctat taatattgtc aggaagacta 240
aagtgcagca tagactaaga atgaggaaaa ttcctagact nnaatagtat aaggagaggg 300
tttacctact atttgaggca gttggtctaa tagtaagcaa tcacagggag aaagcagaac 360
tacttaactc ttctgtgttg aggaatgaca taaaaggtag gaaggatata acaaatgttg 420
ataagaggag tctgatggat gagaggaggg aactgcttta aatgagttct acttcagaca 480
tadgttaatt ctcagagccc acaaaacttt cacttttatt tg 522

<210> 122
<211> 666
<212> DNA
<213> Gorilla

<220>
<221> misc_feature
<222> (1)...(666)
<223> n = A,T,C or G

<400> 122
cattatgacn nnnnnnnatt taattgcaga ggtaggtatg aatgtdctgt actatgttgt 60
ataacttaaa cccgatagac tgtatcttac tgtcataaca ataatgagtc atctagatta 120
tcgagtgaga tacatattta tcttaagaat tatctttaaa aatttcaaaa attttaattt 180
tactcttgtg ttttaggaaa aaagtattgc ataaagctat taatattgtc aggaagacta 240
aagtgcagca tagactaaga atgaggaaaa ttcctagact nnnaatagta taaggagagg 300
gtttacctac tatttgaggc agttggtcta atagtaagca atcacaggga gaaagcagaa 360

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ctacttaact cttctgtgtt gaggaatgac ataaaaggta ggraaggata taacaaatgt 420
tgataagagg rgtctgatgg atgagaggag ggaactgctt taaatgagtt ctacttcaga 480
cataagttaa ttctcagagc ccacaaaaac tttcactttt atttgtgaaa tgcaactcag 540
ttctcatggc ttaacacttt aamccatgag agactgaaga gttgagaagc ttggcagatg 600
ctgctgtgat agtcaaaaag aaagtgggtg ccatgagcta ctattgatgt atttgccatt 660
gatccc                                                            666

<210> 123
<211> 741
<212> DNA
<213> Orang-utan

<220>
<221> misc_feature
<222> (1)...(741)
<223> n = A,T,C or G

<400> 123
cattatgacn nnnnnaaatt taattgcaga ggtaggtacg aatgtactgt gctatgttgt 60
ataacttaaa cacaatagac tgtatcttac tgtcataaca ataatgactc atctagatta 120
ttgagtgaga tacatattta tcttaagawt tatcttaaaa aatttcagaa aatttaattt 180
tactgttgtg ttttaggaaa aacgtattgc ataaagctat taatattgtc aggaaaagtg 240
cagagtagac taagaattag gaaaattcct agactaaaan nnnataagga gagggtttac 300
ctactgtttg aggcagttgg tctaatagta agcgattata gggagaaagc agaactactt 360
aactcttctg tgttgaggaa tgacatgaaa ggtaggaaag gatataacaa atgttgataa 420
gaggagcctg atggatgaga ggagggaact gctttaaatg agttctactt cagacataag 480
ttaattctca gagcccacaa aaactttcac tttcatttgt gaaatacaac tcagttctca 540
cggcttaaca ctttaaacca tgagagaact gaagagttga gaagcttggc agatgcttct 600
gtgatagtca aaaagaaagt gggtgccatg agctactatt gatgtatttg ccattgatcc 660
cycctgaaaa tctagaatgg actttcagac aaatggtttg aaaatcctaa atcactaatg 720
attgggattt agtatagatt c                                           741

<210> 124
<211> 608
<212> DNA
<213> Orang-utan

<220>
<221> misc_feature
<222> (1)...(608)
<223> n = A,T,C or G

<400> 124
cattatgacn nnnncaaatt taattgcaga ggtaggtacg aatgtactgt gctatgttgt 60
ataacttaaa cacaatagac tgtatcttac tgtcataaca ataatgactc atctagatta 120
ttgagtgaga tacatattta tcttaagaat tatcttaaaa datttcagaa aatttaattt 180
tactgttgtg ttttaggaaa aacgtattgc ataaagctat taatattgtc aggaaaagtg 240
cagagtagac taagaattag gaaaattcct agactaaaat nnnataagga gagggtttac 300
ctactgtttg aggcagttgg tctaatagta agcgattata gggagaaagc agaactactt 360
aactcttctg tgttgaggaa tgacatgaaa ggtaggaaag gatataacaa atgctgataa 420
gaggagcctg atggatgaga ggagggaact gctttaaatg agttctactt cagacataag 480
ttaattctca gagccacaaa aactttcact ttcatttgtg aaatacaact cagttctcac 540
ggcttaacac tttaacccat ggagagacct gaagagttgg agaagcttgg cagatgcttc 600
tgtgatag                                                          608

<210> 125
<211> 402
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<212> DNA
<213> Banting cattle

<400> 125
gagagacatt atgacaccgc caaatttaat tgcagaggta agtataggta cacatattat 60
gttagataac ttgaagccaa cagtctaaat tttactgtca taccaataat gaataatctc 120
aagtattaag tgatatattt atcttaaaga tggtctgaga aaatttgaaa ttaattttgc 180
tgttgtgttt ttggaaataa gtatcatgta aatgaggaag actaaattga attaactgaa 240
aactaggaga aatttataga ctaacagaat aaatagaggg ttatatctgt gatttgaggc 300
atttggcatg atagtaagag attacaggga gaaaggagaa tggcttaatt ctgtaatgga 360
acatgacctg tacagtggaa aagggtataa tgaaatatgg at 402

<210> 126
<211> 479
<212> DNA
<213> Indian elephant

<220>
<221> misc_feature
<222> (1)...(479)
<223> n = A,T,C or G

<400> 126
gacattatga cnnnnnnnnn nnnnnntgca gaggtaggta taaatgtttt atagtatgtt 60
gtataactta aaaccaaaag tctaaatatt actgccatag caatagtgaa tattctagat 120
tattaagtaa gataaatatt tatcttaagg atggtcttaa aaatttgagg gaaataaatt 180
taattttaat attatgtttt agaacaagta tcccataacc ctatgagtaa tgtcgtgaag 240
accaaaataa agaataggct aagaattagg agaaattcct aggataagaa taaaataagg 300
aagggggca tgcctagtgt ttgaggcagt tggtgtaata ctaagagatt atatggagaa 360
agcaggacta ctcaattctt ctctatcaaa gagaataacc taaagggtgg aaaagagtat 420
aacaaatgtg gataagagga gcttgagaac gagagtgggg agatgcttta aatgagctc 479

<210> 127
<211> 284
<212> DNA
<213> Fishing cat

<400> 127
gagagacatt atgacaccgc caaatttaac tgcagaggta ggtattaaht gcagagtaat 60
gtattatgtt atataactyc aaaccagtag actaaatctt actgtcatag cagtgatgaa 120
taatctcatt attaagtgag ataaatattt atcttcaaga tggtcttaaa aaatttgcaa 180
aacaaattta attttgctgt tgtgttttgg gaagcaagta tcctataaac ctgccggtac 240
taactagtag gaagactaat cccagagtag actaagaatt tgga 284

<210> 128
<211> 290
<212> DNA
<213> Sun bear

<220>
<221> misc_feature
<222> (1)...(290)
<223> n = A,T,C or G

<400> 128
gagagacatt atgacnnnnn nnnnnnnaac tgcagaggta ggtaaaaact gccaagtaat 60
gtatttatgt tgtataactt aaaaccagta gaccaaatct tactatcata gcagtaatga 120

ataatctcaa ttaattaagt ggaagtaaat tatttatctt aaagatggtc ttagacactt 180
tggaaaacta atttaatatt gctgttgtgt tttaggaagc agttatcata taaacctgcc 240
agtactagta cgaatactaa aacgcagagt agactctaaa attgaggaaa 290

<210> 129
<211> 272
<212> DNA
<213> Dwarf goat

<400> 129
gagagacatt atgacaccgc caaatttaat tgcagaggta agtacaggta cacatattat 60
gttaggtaac ttgaagccaa cagtctaaat tttactgtca taccaataat gaataatcac 120
aagtattaag taatatattt atgttaaaga tggcctgaga aaatgtgaaa ttaactttgc 180
tgttgtgttt ttggaaataa gtatcatgta aatgaggatg actaaattga attaactgaa 240
aactaggaga agtttataga ctaacagaat ag 272

<210> 130
<211> 327
<212> DNA
<213> Guinea pig

<220>
<221> misc_feature
<222> (1)...(327)
<223> n = A,T,C or G

<400> 130
gagagacatt atgacnnnnn nnnatttaat tgcagaggta tgtataaata taccatggtc 60
tggggtatga ttgaaaacca ataggctgtg ttttattatc agcaataatg gatcatttaa 120
attattagaa aagataaata tttttcttta attatagtct gagataattt gaaaatacta 180
attttttggt tgagctttag aaatcatgtg tcaggtaaat ctgtcaatgt tgtccggaaa 240
actcgagtac atagtagact taagaattag gataaattac taaactgata atggaataaa 300
gaggatattt acctgctgct tgaaaca 327

<210> 131
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Zoo43sUV

<400> 131
tgtgctgaga gacattatga c 21

<210> 132
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Zoo44aRV

<400> 132
ttgtctctgg tccttactt 19

<210> 133

<211> 281
<212> DNA
<213> Man

<400> 133
ttgtctctgg tccttacttc cccatagaaa tctagggcct cttgtgcctt taaaaatttg 60
ccccgatgta ataaatatgc ataaatcatt ataccagttc gtccctttcc agctttacag 120
tgaattgctg caacatgatt gtcatcttca cttagccatt ggtcaagatc ttcacaaaag 180
ggtttgataa gttctagctg tggtgggtta tggtcttcaa aaggatattg cgcaactctg 240
taattagatt tggcggtgtc ataatgtctc tcagcacaac t 281

<210> 134
<211> 271
<212> DNA
<213> Chimpanzee

<400> 134
ggtccttact tccccataga aatgtagggc ctcttgtgcc tttaaaaatt tgccccgatg 60
taataaatat gcataaatca ttataccagt tcgtcccttt ccagctttac agtgaattgc 120
tgcaacatga ttgtcatctt cacttagcca tcggtcaaga tcttcacaaa agggtttgat 180
aagttctagc tgtggtgggt tatggtcttc aaaaggatat tgcgcaactc tgtaattaga 240
tttggcggtg tcataatgtc tctcagcaca a 271

<210> 135
<211> 271
<212> DNA
<213> Oran-utan

<220>
<221> misc_feature
<222> (1)...(271)
<223> n = A,T,C or G

<400> 135
tggtccttac ttccccatag aaatctaggg cctcttgtgc ctttaaaaat ttgccccgat 60
gtaataaata tgcacaaatc attacaccag ttcgtccctt tccagcttta cagtgaattg 120
ctgcaacatg attgtcatct tcacttagcc attggtcaag atcttcacaa aagggtttga 180
taagttctag ctgtggtggg ttatggtctt caaaaggata ttgtgcaact nnnnnnnnnn 240
nnnnnnnnnn gtcataatgt ctctcagcac a 271

<210> 136
<211> 268
<212> DNA
<213> Gorilla

<400> 136
ctggtcctta cttccccaga gaaatctagg gcctcttgtg cctttaaaaa tttgccccga 60
tgtaataaat atgcataaat cattatacca gttcgtccct ttccagcttt acagtgaatt 120
gctgcaacat gattgtcatc ttcacttagc cattggtcaa gatcttcaca aaagggtttg 180
ataagttcta gctgtggtgg gttatggtct tcaaaaggat attgtgcaac tctgcaatta 240
aatttggcgg tgtcataatg tctctcag 268

<210> 137
<211> 306
<212> DNA
<213> Domestic pig

<400> 137
tctctggtcc ttacttcccc atagaaatct tgtgccttta aaaatttgcc cggatgaaac 60
aaatatgcac aaatcattac accagttcat ccttttccag gtttacagtg aattgctgca 120
acatgattgt catcttcact tagccattgg tcaagatctt cacaaaaagg tttgataaat 180
tctagctgtg gtggattatg atcttcaaaa ggatactgtg caactctgca gttaaatgtg 240
gcggtgtcat aatgtctctc agcacaactc tgcaattaaa tttggcggtg tcataatgtc 300
tctcag 306

<210> 138
<211> 258
<212> DNA
<213> Wild boar

<400> 138
tctctggtcc ttacttcccc atagaaatct tgtgccttta aaaatttgcc cggatgaaac 60
aaatatgcac aaatcattac accagttcat ccttttccag gtttacagtg aattgctgca 120
acatgattgt catcttcact tagccattgg tcaagatctt cacaaaaagg tttgataaat 180
tctagctgtg gtggattatg atcttcaaaa ggatactgtg caactctgca gttaaatgtg 240
gcggtgtcat aatgtctc 258

<210> 139
<211> 18
<212> DNA
<213> SPL5 senseArtificial Sequence

<220>
<223> SPL5 sense

<400> 139
aaatttaatt gcagaggt 18

<210> 140
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Zoo44aRV antisense

<400> 140
ttgtctctgg tccttacttc 20

<210> 141
<211> 712
<212> DNA
<213> Man

<400> 141
ttgtctctgg tccttacttc cccatagaaa tctagggcct cttgtgcctt taaaaatttg 60
ccccgatgta ataaatatgc acatatcatt acaccagttc gtccctttcc agctttacag 120
tgaattgctg caacatgatt gtcatcttca cttagccatt ggtcaagatc ttcacaaaag 180
ggtttgataa gttctagctg tggtgggtta tggtcttcaa aaggatattg tgcaactgtg 240
gtaaaaagat aacctcagaa taagaaaaaa aaactcttga atttttaatt aacaagtagg 300
taactttaga aatgttgcat acaaacttaa caggtattta aaagaaacac tggattccag 360
agaaaaataa tgtattgctt aactttctaa ttgttaaata gaaaatagtc tcttgataag 420
tcttaaatat aatcattaag gaagccaggt attattttcc cccattttat tcaggaggat 480
atattctggg aatttacgct atacggactg gtagcatagg tcacatatta gaggtagagc 540

taaacccaaa atgaactgtc acatggacat ttcgtcagga ctctcaatgc aaaaggaata 600
atactattta tagtatttat ttcatcatca caaaacatat tccaaagaca gaatagttta 660
ctaataggta aactatgcaa agaactacat attacatttc ataaaataaa aa 712

<210> 142
<211> 593
<212> DNA
<213> Chimpanzee

<220>
<221> misc_feature
<222> (1)...(593)
<223> n = A,T,C or G

<400> 142
tggtccttac ttccccatag aaatctaggg cctcttgtgc ctttaaaaat ttgccccgat 60
gtaataaata tgcacaaatc attacaccag ttcgtccctt tccagcttta cagtgaattg 120
ctgcaacatg attgtcatct tcacttagcc attggtcaag atcttcacaa aagggcttga 180
taagttctag ctgtggtggg ttatggtctt caaaggata ttgtgcaact gtggtaaaaa 240
gataacctca gaataagaaa aaaaaactct tgaattttta attancaagt aggnnnnttt 300
agaatgttgc atacaaactt aacaggtatt taaaagaaac actggattcc agagaaaaat 360
aatgtattgc ttaactttct aattgttaaa tagaaaatag tctcttgata agtcttaaat 420
ataatcatta aggaagccag gtattattct cccccatttt attcaggagg atatattctg 480
ggaatttacg ctatacggac tggtagcata ggtcacatat tagaggtaga gctaaactca 540
aaatgaactg tcacatggac atttcatcag gactctcaat gcaaaaggaa taa 593

<210> 143
<211> 589
<212> DNA
<213> Chimpanzee

<220>
<221> misc_feature
<222> (1)...(589)
<223> n = A,T,C or G

<400> 143
ccttacttcc ccatagaaat ctagggcctc ttgtgccttt aaaaatttgc cccgatgtaa 60
taaatatgca caaatcatta caccagttcg tccctttcca gctttacagt gaattgctgc 120
aacatgattg tcatcttcac ttagccattg gtcaagatct tcacaaaagg gtttgataag 180
ttctagctgt ggtgggttat ggtcttcaaa aggatattgt gcaactgtgg taaaaagata 240
acctcagaat aagaaaaaaa aactcttgaa tttttaatta acaagtaggn nntttagaaa 300
tgttgcatac aaacttaaca ggtatttaaa agaaacactg gattccagag aaaaataatg 360
tattgcttaa ctttctaatt gttaaataga aaatagtctc ttgataagtc ttaaatataa 420
tcattaaggg agccaggtat tattctcccc cattttattc aggaggatat attctgggaa 480
tttacgctat acggactggt agcataggtc acatattaga ggtagagcta aactcaaaat 540
gaactgtcac atggacattt catcaggact ctcatgcaaa aggaataat 589

<210> 144
<211> 593
<212> DNA
<213> Orang-utan

<400> 144
acttccccat agaaatctag ggcctcttgt gcctttaaaa atttgccccg atgtaataaa 60
tatgcacaaa tcattacacc agttcgtccc tttccagctt tacagtgaat tgctgcaaca 120
tgattgtcat cttcacttag ccattggtca agatcttcac aaaagggttt gataagttct 180

agctgtggtg ggttatggtc ttcaaaagga tattgtgcaa ctgtggtaaa aagataacct 240
cagaataaga aaaaaaaact cctgaatttt tcattaacaa gtaggtaact ttagaaatgt 300
tgcatacaaa cttaacaggt atttaaaaga aacactggat tccaaagaaa aataatgtat 360
tgcttaactt tctaattgtt aaatagaaaa tagtctcttg ataagtctta aatataatca 420
ttaaggaagc caggtattat tttcccccat tttattcagg aggatatatt ctggggattt 480
acactatacg gactggtagc ataggtcaca tattagaggt agagctaaac ccaaaatgaa 540
atgtcacatg gacatttcgt caggactgtc aatgcaaaag gaataatact att 593

<210> 145
<211> 724
<212> DNA
<213> Orang-utan

<400> 145
tccttacttc cccatagaaa tctagggcct cttgtgcctt taaaaatttg ccccgatgta 60
ataaatatgc acaaatcatt acaccagttc gtccctttcc agctttacag tgaattgctg 120
caacatgatt gtcatcttca cttagccatt ggtcaagatc ttcacaaaag ggtttgataa 180
gttctagctg tggtgggtta tggtcttcaa aaggatattg tgcaactgtg gtaaaaagat 240
aacctcagaa taagaaaaaa aaactcctga atttttcatt aacaagtagg taactttaga 300
aatgttgcat acaaacttaa caggtattta aaagaaacac tggattccaa agaaaaataa 360
tgtattgctt aactttctaa ttgttaaata gaaaatagtc tcttgataag tcttaaatat 420
aatcattaag gaagccaggt attattttcc cccattttat tcaggaggat atattctggg 480
aatttacact atacggactg gtagcatagg tcacatatta gaggtagagc taaacccaaa 540
atgaaatgtc acaggacatt tcgtcaggac tgtcaatgca aaaggaataa tactatttat 600
agtattatac atcatcacaa acatattcca aagacagaac agattactaa taggataaac 660
tatggaagac tatatattac atttcataaa ataaaaagct aagtgtgtta tttaaagggg 720
gtct 724

<210> 146
<211> 831
<212> DNA
<213> Gorilla

<400> 146
gtccttactt ccccatagaa atctagggcc tcttgtgcct ttaaaaattt gccccgatgt 60
aataaatatg cacaaatcat tacaccagtt cgtccctttc cagctttaca gtgaattgct 120
gcaacatgat tgtcatcttc acttagccat tggtcaagat cttcacaaaa gggtttgata 180
agttctagct gtggtgggtt atggtcttca aaaggatatt gtgcaactgt ggtaaaaaga 240
taacctcaga ataagaaaaa aaactcctga atttttaatt aacaagtagg taactttaga 300
aatgctgcat acaaacttaa caggtattta aaagaaacac tggattccag agaaaaataa 360
tgtattgctt aactttctaa ttgttaaata gaaaacagtc tcttgataag tcttaaatat 420
aatcattaag gaagccaggt attattttcc cccattttat tcaggaggat atattctggg 480
aatttacgct atatggactg gtagcatagg tcacatatta gaggtagagc taaacccaaa 540
acgaactgtc acatggacat ttcgtcagga ctctcaatgc aaaaggaata atactattta 600
tagtatttat wtcatcatca caaaacatat tccaaagaca gaatagatta ctaataggat 660
aaactatgca aagaactaca tattacattt cataaaataa aaatgctaag tgtgttattt 720
aaaggtggtc ttgcaaatgt tagtgttgta tacacatgta atcattaggg aagccaagta 780
ttattttcct ccgttttctg caggagaata cattctggga atctatgctc a 831

<210> 147
<211> 556
<212> DNA
<213> Domestic pig

<400> 147
tctctggtcc ttacttcccc atagaaatct agggcctctt gtgcctttaa aaatttaccc 60
cgatgtaaca aatatgcaca aatcattaca ccagttcgtc cctttccagc tttacagtga 120

attgctgcaa catgattgtc atcttcactt agccattggt caagatcttc acaaaaaggt 180
ttgataagtt ctagctgtgg tggattatgg tcttcgaaag gatactgtgc aactgtggaa 240
aaagataacc tcagaataaa aaatctctc ctgagttgct aattaaaagt aggttaactt 300
ttgaaatctt gcatataaat tcaatagaga ttttaaataa aaactgaact ccagggaaaa 360
attgtctgat aattttcaaa tagaaaatag aaaataatct cctgttaact caaatttccc 420
cattagatag ggaggccaag tatcattttc cccactttat gaaggaggaa actttgcaat 480
agagtagcaa tgtatcagag gtcacaacgt atcagaaatg gaggtaaact caaaatgaaa 540
tgtcacatga gccctt 556

<210> 148
<211> 752
<212> DNA
<213> Wild boar

<400> 148
tctctggtcc ttacttcccc atagaaatct agggcctctt gtgcctttaa aaatttaccc 60
cgatgtaaca aatatgcaca aatcattaca ccagttcgtc cctttccagc tttacagtga 120
attgctgcaa catgattgtc atcttcactt agccattggt caagatcttc acaaaaaggt 180
ttgataagtt ctagctgtgg tggattatgg tcttcgaaag gatactgtgc aactgtggaa 240
aaagataacc tcagaataaa aaatctctc ctgagttgct aattaaaagt aggttaactt 300
ttgaaatctt gcatataaat tcaatagaga ttttaaataa aaactgaact ccagggaaaa 360
attgtctgat aattttcaaa tagaaaatag aaaataatct cctgttaact caaatttccc 420
cattagatag ggaggccaag tatcattttc cccactttat gaaggaggaa actttgcaat 480
agagtagcaa tgtatcagag gtcacaacgt atcagaaatg gaggtaaact caaaatgaaa 540
tgtcacatga gcccttctta tcagggctta ccatatattt tctaacaaaa ggagttgcag 600
tacttataat attggatcat tacaaaatgt atgtttcaaa gaaagtatag ttcactaata 660
aatcaacaat ggaaaagata gcaatttgtg cttcatacaa taaaaatgcc aagcatgtta 720
ttttaaagat ggtcttgcta atagtgctgt at 752

<210> 149
<211> 715
<212> DNA
<213> Cattle

<400> 149
ctctggtcct tacttcccca tagaaatcta gggcctcttg tgcctttaaa aatttgcccc 60
gatgtaacaa atatgcacaa atcattacac cagttcgtcc ctttccagct ttacagtgaa 120
ttgctgcaac atgattgtca tcttcactta gccattggtc aagatcttca caaaagggtt 180
tgataagttc taactgtggt ggattatggt cttcaaaggg atactgtgca actgtgataa 240
aaaaataacc tcagaataag aaaataatct cacttgaatt gcttattaca agtaggttaa 300
ctttagaaat gttgcataca aatagtttaa aaatatctga actatagaga aaaagaattt 360
attgtctgat aattttctaa ttttgaacag aaaataatct ctcattaact caaatttatc 420
cattagacag gtacgtcaag tattattttc ctcactttat gatggaggca atggagtagc 480
aacatatcag aggtcacaac ataacagagg gagaggtaaa ctcaaaatga tacatcacaa 540
gagcctctta tcagggstct caatacattt tctagcaaaa ggaactgtaa tatctataat 600
attgcattat cacaaaatat gtattccaaa gaaagcaaag atcctaataa atcacaatgc 660
aaagactgca ttttatgcta tatatacaga aggcagcata ttattttaaa gatgg 715

<210> 150
<211> 708
<212> DNA
<213> Banting cattle

<400> 150
ggtccttact tccccataga aatctagggc ctcttgtgcc tttaaaaatt tgccccgatg 60
taacaaatat gcacaaatca ttacaccagt tcgtcccttt ccagctttac agtgaattgc 120
tgcaacatga ttgtcatctt cacttagcca ttggtcaaga tcttcacaaa agggtttgat 180

aagttctaac tgtggtggat tatggtcttc aaagggatac tgtgcaactg tgataaaaaa 240
ataacctcag aataagaaaa taatctcact tgaattgctt attacaagta ggttaacttt 300
agaaatgttg catacaaata gtttaaaaat atctgaacta tagagaaaaa gaatttattg 360
tctgataatt ttctaatttt tgaacagaaa ataatctctc attaactcaa atttatccat 420
tagacaggta cgtcaagtat tattttcctc actttatgat ggaggcaatg gagtagcaac 480
atatcagagg tcacaacata acagagggag aggtaaactc aaaatgatac atcacatgag 540
cctcttatca gggctctcaa tacattttct agcaaaagga actgtaatat ctataatatt 600
gcattatcgc aaaatatgta ttccaaagaa agcaaagatc actaataaat caacaatgca 660
aaagactgca ttttatgcta tatatacaga aggcaagcat attatttt 708

<210> 151
<211> 548
<212> DNA
<213> Red buffalo

<400> 151
ggtccttact tccccataga aatctagggc ctcttgtgcc tttaaaaatt ttccccgatg 60
taacaaatat gcacaaatca ttacaccagt tcgtcccttt ccagctttac agtgaattgc 120
tgcaacatga ttgtcatctt cacttagcca ttggtcaaga tcttcacaaa agggtttgat 180
aagttctaac tgtggtggat tatggtcttc aaagggatac tgtgcaactg tgataaaaag 240
ataacctcag aataagaaaa taatctcact tgaattgctt attacaagta ggttaacttt 300
agaaatgttg catacaaaga gtttaaaaat atctgaacta tagagaaaaa gaatttattg 360
tctgataatt ttctaatttt gaacagaaaa taatctctca ttaactcaaa tttatccatt 420
agacaggtaa gtcaagtatt attttcctca ctttatgatg gaggcaatgg gtagcaacat 480
atcagaggca caacataaca gaggggaaag gtaaactcaa aatgaaacat cacatgagcc 540
tcttatca 548

<210> 152
<211> 700
<212> DNA
<213> Sheep

<400> 152
tctggtcctt acttccccat agaaatctag ggcctcttgt gcctttaaaa atttgccccg 60
atgtaacaaa tatgcacaaa tcattacacc agttcgtccc tttccagctt tacagtgaat 120
tgctgcaaca tgattgtcat cttcacttag ccattggtca agatcttcac aaaagggttt 180
gataagttct aactgtggtg gattatggtc ttcaaaggga tactgtgcaa ctgtgataaa 240
aagataaccg cagaataaga aaataatctc acttgaattg cttattacaa gtaggctaac 300
tttagaaatg ttgcatacaa atagtttaaa aatrtctraa ctatagagga aaagaattta 360
ttgtctgata attttctaat tttcgaacag aaaataatct ctcattaact caaatttatc 420
cattcgacag gtaagacaag tattattttc ctcactctat gatggaggca atggaggagc 480
aacatatcag aggtcacaac ataacggagg aagaggcaaa ctcagaatga aacgtcgcac 540
gagcctctta gcagggctct caatacgttt cctagcaaaa ggaactgtaa catctataat 600
atcgcattat cacaaaacat gtattccaaa gaaagtacag atcactaata agtcaacaat 660
gcagaagact gcattttatg cttgacgtga cagaaaggca 700

<210> 153
<211> 780
<212> DNA
<213> Bighorn

<400> 153
ccttacttcc ccatagaaat ctagggcctc ttgtgccttt aaaaatttgc cccgatgtaa 60
caaatatgca caaatcatta caccagttcg tccctttcca gctttacagt gaattgctgc 120
aacatgattg tcatcttcac ttagccattg gtcaagatct tcacaaaagg gtttgataag 180
ttctaactgt ggtggattat ggtcttcaaa gggatactgt gcaactgtga taaaaagata 240
accgcagaat aagaaaataa tctcacctga attgcttatt acaagtaggc taactttaga 300

aatgttgcat acaaatagtt taaaaatatc tgaactatag tggaaaagaa tttattgtct 360
gataattttc taattttcga acagaaaata atctctcatt aactcaaatt tatccattcg 420
acaggtaaga caagtattat tttcctcact ctatgatgga ggcaatggag gagcaacata 480
tcagaggtca cagcataacg gaggaagagg caaactcaga atgaaacgtc gcacgagcct 540
cttagcaggg ctctcaatac gtttcctagc aaaaggaact gtaacatcta taatatcgca 600
ttatcacaaa acatgtattc caaagaaagt acagatcact aataagtcaa caatgcagaa 660
gactgcattt tatgcttgac gtgacagaaa gggcaagcat attatttaaa gatggtctcg 720
aaaatgcaac tgttgcgtac acacaattct aaagacattc acaaagacac ttaaaaattt 780

<210> 154
<211> 463
<212> DNA
<213> Cameroon sheep

<400> 154
acttccccat agaaatctag ggcctcttgt gcctttaaaa atttgccccg atgtaacaaa 60
tatgcacaaa tcattacacc agttcgtccc tttccagctt tacagtgaat tgctgcaaca 120
tgattgtcat cttcacttag ccattggtca agatcttcac aaaagggttt gataagttct 180
aactgtggtg gattatggtc ttcaaaggga tactgtgcaa ctgtgataaa aagataaccg 240
cagaataaga aaataatctc acttgaattg cttattacaa gtaggcggct ttagaaatgt 300
tgcatacaaa tagtttaaaa atgtctgaac tatagaggaa agaatttatt gtctgataat 360
tttctaattt tcgaacagaa aataatctct cattaactca aatttatcca ttcgacaggt 420
agacaagtat tattttctca ctctwtgatg gaggcattgg agg 463

<210> 155
<211> 524
<212> DNA
<213> Deer

<400> 155
tctctggtcc ttacttcccc gtagaaatct agggcctctt gtgcctttaa aaatttgccc 60
cgatgtaaca aatatgcaca aatcattaca ccagttcgtc cctttccagc tttacagtga 120
atcgctgcaa catgattgtc atcctcactt agccattggt caagatcttc acaaaagggc 180
ttgataagtt ctaactgtgg tggattatgg tcttcaaagg gatactgtgc aactgtgata 240
aaaaaatgac ctcagaataa gaaaataatt tcacttgaat tgcttattac aagtaggtta 300
actttagaaa tgttgcatat aaatagttta aaaatatccg aaccataaag aaaaagaatt 360
tattgtctgg taattttcta atttttgaac agaaaataat ctctcattaa ctcaaattta 420
tccattagaa aggtaagtca agtattgttt tcctcacttc atgatggagg caatggagga 480
gcaacatatc agaggcacag cataacagag gaagaggtaa actc 524

<210> 156
<211> 647
<212> DNA
<213> Roe deer

<400> 156
tctctggtcc ttacttcccc gtagaaatct agggcctctt gtgcctttaa aaatttgccc 60
cgatgtaaca aatatgcaca aatcattaca ccagttcgtc cctttccagc tttacagtga 120
atcgctgcaa catgattgtc atcttcactt agccattggt caagatcttc acaaaagggt 180
ttgataagtt ctaactgtgg tggattatgg tcttcaaagg gatactgtgc aactgtgata 240
aaaagataac ctcagaataa gaaaataatt tcacttgaat tgcttattac aagtaggtta 300
actttagaaa tgttgcatac aaatagttta aaaatatcca aaccataaag aaaagaattt 360
attgtctgat aattttctaa tttttgaaca gaaaataatc tcttatwaac tcaaatgtat 420
ccattagaaa ggtaagcaga gtattgtttt cctcacttca tgatgcaggc aatggaggag 480
caacatatca gaggtcacag cataacagag gaagaggtaa actcacaatg aaacatcaca 540
tagcctctta tcaggactct caatacattt tctagcagaa ggaaccgtaa tatctataac 600

attgcattat cacaaagtat gtattccaaa taaagtacat aacacta 647

<210> 157
<211> 512
<212> DNA
<213> Goitred gazelle

<400> 157
tccttacttc cccatagaaa tctagggcct cttgtgcctt taaaaatttg ccccgatgta 60
acaaatatgc acaaatcatt acaccagttc gtccctttcc agctttacag tgaattgctg 120
caacatgatt gtcatcttca cttagccatt ggtcaagatc ttcacaaaag ggtttgataa 180
gttctaactg tggtggatta tggtcttcaa agggatactg tgcaactgtg ataaaaagat 240
aacctcagaa taagaaaata atctcacttg aattgcttat tataagtagg ttaactttat 300
aaatgttgca tacaaacagt ttaaaaatat ctgaactaca gagaaaaaga atttattgtc 360
tgataatttc taattttttg acagaaaata atctctcata actcaaattt acccattaga 420
caggtaagcc aagtattatt ttctcacttt atgatggagg caatggagta gcacatatca 480
gaggcacaac ctaacagagg agaggtaact ca 512

<210> 158
<211> 798
<212> DNA
<213> Horse

<400> 158
ggtccttact tctccataga aatctagggc ctcctgtgcc tttaaaaact tgccccgatg 60
taacaaatat gcacaaatca ttacaccagt tcgtcccttt ccagctttac agtgaattgc 120
tgcaacatga ttgtcatctt cacttagcca ttggtcaaga tcttcacaaa agggtttgat 180
aagttctagc tgtggtggat tatgatcttc aaaaggatac tgtgcaactg tggtaaaaag 240
ataatctcaa attaagaaaa aaatctctcc tgaattgttt attaaaagta ggttaacttt 300
aggaatgctg cgtataagtt taacagatat ttaaaagaaa aactgaactc cagagaaaaa 360
taatttattg tctgataatt ttctaatttt tgaatagaaa ataagagtcc cattaattct 420
caaaactcat ccattagaca gggaagccaa gtattatttt ccctactcta tgaaggagta 480
cattgtgcta tgcagaggta gcaaaggtca caacacataa gacatggagg tgaactcaaa 540
atgaaatgtc acatgggcct cttgttatgg ctttcaatgc atactctaac aaaaggagaa 600
ataacactta gaatattgca tcaccacaaa acatatattc caaagaaagt acagattact 660
aataaatcaa cggraaggat ggcattttac acttcatata ataaaaatgc taactgtgtt 720
attttaaaga tggtctggca aatggtagcg ctgtataccg actttaacag catttacaaa 780
gaaactggaa aatcactt 798

<210> 159
<211> 519
<212> DNA
<213> African elephant

<220>
<221> misc_feature
<222> (1)...(519)
<223> n = A,T,C or G

<400> 159
tggtccttac ttcnnnnnnn nnnnnnnnnn nnncttgtgc ctttaaaaat ttgccccgat 60
gtaacaaata tgcacaaatc attacaccag ttcgtccctt tccagcttta cagtgaattg 120
ctgcaacatg attgtcatct tcacttagcc attggtcaag atcttcacaa aagggtttga 180
taagctctag ttgtggtggg ttgtggtctt caaaaggata ctgtgcaact gtggtaaaaa 240
gataaactca gaataagaaa aaaatctctc ctgaattttt aattaaaagt aggttagctt 300
cagaaacatt gcacataaac tataaacagg tgtttaaata aaagataagc taaactccct 360
taaaaaaaaa tttattgcct gataacttgc tagtttttga atatagtctc tcactaactc 420

ttaaatgcat ccattaaaaa aggagaccaa gtattatttt ccccacatta tgctagagga 480
aactgtgtta tgctgaagta gcacaggtta catctcaga 519

<210> 160
<211> 776
<212> DNA
<213> Indian elephant

<220>
<221> misc_feature
<222> (1)...(776)
<223> n = A,T,C or G

<400> 160
tggtccttac ttccccataa aaatctaggg cttcttgtgc ctttaaaaat ttgccccgat 60
gtaacaaata tgcacaaatc attacaccag ttcgtccctt tccagcttta cagtgaattg 120
ctgcaacatg attgtcatct tcacttagcc attggtcaag atcttcacaa aagggtttga 180
taagctctag ttgtggtggg ttgtggtctt caaaaggata ctgtgcaact gtggtaaaaa 240
gataaactca gaataagaaa aaaatctctc ctgaattttt aattaaaagt aggttagctt 300
cagaaacatt gcacataaac tataaacagg tgtttaaata aaagataagc taaactccat 360
taaaaaaaaa tttattgcct gataacttgc tagtttttga atatagtctc tcactaactc 420
ttaaatgcat ccattaaaaa aggagaccaa gtattatttt ccccacatta tgctagagga 480
aactgtgtta tgctgaagta gcacaggtta catctcagag gtggagctga acccaaaaag 540
aaatgttaca taggcctctt gtcaagggct gtcaatgcat tttctaacaa aaggagtagt 600
gacactaata atattgcatc accttggtaa cagaacatat tctcaaaggt agaatggatt 660
attaacagaa tcagtaatgg aaaggattgc attttatact tcatataaaa natgttcggt 720
ctattattta aaggtggcct tacaaatgtt agtgttgtat acaatgattt ataaga 776

<210> 161
<211> 701
<212> DNA
<213> Dog

<400> 161
ggtccttact tccccataga aatctagggc ctcttgtgcc tttagaaatt tgccccgatg 60
taataaatat gcacaaatca ttacaccagt tcgtcccttt ccagctttac agtgaattgc 120
tgcaacatga ttgtcatctt cacttagcca ttggtcaaga tcttcacaaa agggtttgat 180
aagttctagc tgtggtggat tatggtcttc aaaaggatac tgtgcaactg tggtaaaaag 240
ataacctcag aattagaaaa aagtctttcc tgaactgttt attaaaagta ggttaacttt 300
agaaacattg catgtaagct taacagatgt ttaaaagaaa aacggaactc cagagaaaaa 360
taatttgctg tctgataatt ttccaatttt tgaatagaaa atagtctctc attaattctt 420
aaacctacca ctagagagag aggctaagca ttattttccc cactttaatg aaagaggaaa 480
ctttgcaatg gagagggagc acacgtcaac atatcagagg gaagaggcaa actcaaaatg 540
aaatggcaca caggtttcct gtcagggctc tcaatgcatt ttctgacaaa aggagtcata 600
atatttataa tactacgtca tcacaaaata tatattccag agaaagtata aataaccgat 660
aaatcaatga tggaaaggat tgattttaca cttgatataa t 701

<210> 162
<211> 603
<212> DNA
<213> Sun bear

<220>
<221> misc_feature
<222> (1)...(603)
<223> n = A,T,C or G

<400> 162
ggtccttact tcnnnncata gaaatctagg gcctcttgtg cctttaaaaa tttgccccga 60
tgtaataaat atgcacaaat cattacacca gttcgtccct ttccagcttt acagtgaatt 120
gctgcaacat gattgtcatc ttcacttagc cattggtcaa gatcttcaca aaagggtttg 180
ataagttcta gctgtggtgg attatggtct tcaaaaggat actgtgcaac tgtggtaaaa 240
ggataacctc agaattagaa aaaagtcttt cctgaattgt ttattaaaga aggttaactt 300
tagaaatgtt gcatataagc ttaacagatg tttaaaagaa aaactaaact ccagagaaaa 360
taatttgctg cctgacaatt tacgaatttt tgaatagaaa acagtctctc attaattctt 420
aaacccaccc acaagacaga ggccaagcat tatgttcccc acttaactga agaggaaaga 480
aactttgcta tggagaggta gcacaagtca catatcagag ggagaggcaa attcnaaatg 540
aaatgtcacg taggtaggtt tctgttaggg ctctcaatgc atttttctga caaaaggagt 600
cgt 603

<210> 163
<211> 536
<212> DNA
<213> Mouse

<400> 163
ccttacttcc ccataaaaat ctagggcctc ttgtgccttt aaaaatttgc cccgatgcaa 60
taaatatgca caaatcatta caccagtccg tccctttcca gctttacagt gaattgctgc 120
aacatgattg tcatcttcac ttagccattg gtcaagatct tcacagaagg gtttgataag 180
ttctagctgt ggtgggttat ggtcttcaaa aggatactgt gcaactgttg caaaaagata 240
atcccagtgt aagaaaattt taaatttttt atttaaaaac ataggttaac tttcaaaatg 300
ttatatataa acttactggt tcttaaaaga agcctaactt tcaggaaatt ttaatttatt 360
actaattaaa cctagatttt aaagaaagtc ttttattaat tcttaaatgc attcattaga 420
catggaaaca agcattgtgc tcttcactcc agggaggatg aatctgtgca tgaagggaac 480
acgtcatagc ctatcagtcc actgaatcca aatgcacgtc acccaggcac ttgtca 536

<210> 164
<211> 696
<212> DNA
<213> Guinea pig

<400> 164
acttctccat agaaatctag agcctcttgt gcctttaaaa atttgccccg atgtaataaa 60
tatgcacaaa tcattacacc agtccgtccc tttccagctt tacagtgaat tgctgcaaca 120
tgattgtcat cttcacttag ccattggtca agatcttcac aaaaaggctt gataagttct 180
agctgtggtg ggttatgatc ttcaaaaggg tattgtgcaa ctgtgataaa aacataatct 240
cagagtaaga aagggatctt gcctaaattt ctaatcagaa ataggtcaac tttagaaatg 300
tttcacataa actcaagatg tttaaacaga aaaactgaac tgcatagaaa aataatttat 360
tgttcgttta ctttttact ttcttttttt aaaatacaaa atagtctatt agtaactttt 420
aaacgtatct attacacaag gtggccaggt attacgttct tcacttcatg caggagaaaa 480
ctgtgatttg acagggaaca cagatcataa aacatcaaag atacatcgaa tccaaaaaaa 540
taccaggtca cacagcctct cataacgtct ttaggtgaat ttctgacaaa agcagtaaca 600
tttattatac tgcatcacca tacaacacac tttgaaggaa gtatgaacta ctaatrggat 660
acactatgaa aaarmtgcat tttatatttt ataaat 696

<210> 165
<211> 695
<212> DNA
<213> Himalaya-Tahr

<220>
<221> misc_feature
<222> (1)...(695)
<223> n = A,T,C or G

<400> 165
acttcnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnna atttgccccg atgtaacaaa 60
tatgcacaaa tcattacacc agttcgtccc tttccagctt tacagtgaat tgctgcaaca 120
tgattgtcat cttcacttag ccattggtca agatcttcac aaaagggttt gataagttct 180
aactgtggtg gattatggtc ttcaaaggga tactgtgcaa ctgtgataaa aagataaccg 240
cagaataaga aaataatctc acttgaattg cttattacaa gtaggttaac tttagaaatg 300
ttgtatacaa atagtttaaa aatatctgaa ctatagagga aaagaattta ttgtctgata 360
atttctaat tttgaacaga aaataatctc tcattaactc aaatttatcc attcgacagg 420
taagacaagt attcttttcc tcactctatg atggaggcaa tggaggagca acatatcaga 480
ggtcacaaca taacgsagga agaggcaaac tcaagagtga aacgtcgcac gagcctctta 540
tcaggcctct ccaatacgtt tcctagcaaa aggaactgta acatctataa tatcgcatta 600
tcacaaaaca tgtattccaa agaaagtaca gatcactaat aggtccaatg cagaagactg 660
cattttatgt tgatgtgaca gaaaggcaaa gcata 695

<210> 166
<211> 281
<212> DNA
<213> Human

<400> 166
ccttacttcc ccatagaaat ctagggcctc ttgtgccttt aaaaatttgc cccgatgtaa 60
taaatatgca caaatcatta caccagttcg tccctttcca gctttacagt gaattgctgc 120
aacatgattg tcatcttcac ttagccattg gtcaagatct tcacaaaagg gtttgatcag 180
ttctagctgt ggtgggttat ggtcttcaaa aggatattgt gcaactgtgg taaaaagata 240
acctcagaat aagaaaaaaa actcctgaat ttttaattac a 281

<210> 167
<211> 373
<212> DNA
<213> Vikunja

<220>
<221> misc_feature
<222> (1)...(373)
<223> n = A,T,C or G

<400> 167
ccttacttcn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnngatgtaa 60
caaatatgca caaatcatta caccagttcg tccctttcca gctttacagt gaattgctgc 120
aacatgattg tcatcttcac ttagccattg gtcaagatct tcacaaaagg gtttgataag 180
ttctagctgt ggtggattat ggtcttcaaa aggatactgt gcaactgtgg ttaaaaaaaa 240
agaaaagaaa aaaagaacct cagaataaga aaaaaaatct cccctgaact gcttattaaa 300
tgcaagttaa ctttggaaat gttggcatat taaccttaac agacgtttta aaaggaaaat 360
ctgaactcca gag 373

<210> 168
<211> 291
<212> DNA
<213> Spotted mustang

<220>
<221> misc_feature
<222> (1)...(291)
<223> n = A,T,C or G

<400> 168
ctctggtcct tacttcccca tagaaatcta gggcctcttg tgcctttaaa aatttgcccc 60

gatgnaataa atatgcacaa atcattacac cagttcgtcc ctttccagct ttacagtgaa 120
ttgctgcaac atgattgtca tcttcactga gccattggtc aagatcttca caaaagggtt 180
tgataagttc cagctgcggt gggttatggt cttcaaaagg atactgtgca actgtgtaaa 240
aagatcacct cagagtgaga aaagagtcct tcctgaactg tttcttaaaa g 291

<210> 169
<211> 598
<212> DNA
<213> Fishing cat

<400> 169
acttccccat agaaatctag ggcctcttgt gcctttaaaa atttgccccg atgcaataaa 60
tatgcacaaa tcattacacc agttcgtccc tttccagctt tacagtgaat tgctgcaaca 120
tgattgtcat cttcactgag ccattggtca agatcttcac aaaagggttt gataagttcc 180
agctgcggtg ggttatggtc ttcaaaagga tactgtgcaa ctgtgtaaaa agatcacctc 240
agaatgagaa aagaggcctt cctgaattgc ttcttaaaag taggttaact tcagaaacgt 300
tgcatataag cttaacagat gtttagaagg aaaactaaac tccagagaaa aatactcgtc 360
tgatgatttt ccaatttttg aacagaaaac agtctctcat taatttttaa acctatgcac 420
tagacagaga ggccgattat ttccccccat gacgaagagg agactgctct ggagagcaag 480
cacaagtcac aacgtgtcag agggagagga ggacccggaa tgtcacacag gtttcctgtc 540
agggctctca atgcattttc tgacaaaatg agtaatacgc ttatactatt acatcatc 598

<210> 170
<211> 220
<212> DNA
<213> Turkey

<220>
<221> misc_feature
<222> (1)...(220)
<223> n = A,T,C or G

<400> 170
ctctggtcct tacttcccca tagaaatcta gggcttcttg agcctttaaa aatttgcctc 60
gatgtaataa atatgcacat atcattacac cagttcgtcc ctttccagct ttacagtgga 120
ttgctgcaac atgattgtca tcttcactta gccattggtc aagatcttca caaaanggtt 180
tgataagctc taactgtggt gggttatggt cttcaaaagg 220

<210> 171
<211> 505
<212> DNA
<213> Cockerel

<220>
<221> misc_feature
<222> (1)...(505)
<223> n = A,T,C or G

<400> 171
tctggtcctt acttccccat agaaatctag ggcttcttga gcctttaaaa acttgcctcg 60
atgcaacaaa tatgcacata tcattacacc agttcgtccc tttccagctt tacagtggat 120
tgctgcaaca tgattgtcat cttcacttag ccattggtca agatcttcac aaaaaggttt 180
gataagctct aactgtggtg ggttatggtc ttcaaagggg tactgtgcaa ctgtaatgag 240
aaggattaac ttattaaaat ctaaaaagga taatcaccaa gagctcaact agacaggtca 300
aatttgtgac aagcatgaaa aaattaacat tctaaataca gtcttgcata tagatttgta 360
tacacgcaac tttgattctg ctgttattca gtaacattgc acactaaatg catcacaaat 420
ttctctagta atacgtaagt atcttactgg catgaagagg actatcccac cgtgcttctg 480

nagttnntac tacagactct gcacc 505

<210> 172
<211> 645
<212> DNA
<213> Duck

<220>
<221> misc_feature
<222> (1)...(645)
<223> n = A,T,C or G

<400> 172
ccttacttcc ccatagaaat ctagagcttc ttgagccttt aaaaacttgc ctctatgcaa 60
cagatatgcg catatcatta caccagttcg tccctttcca gctttacagt ggattgctgc 120
aacatgattg tcatcttcac ttagccattg gtcaagatct tcacaaaaag gtttaatgag 180
ctcaagctgt ggtgggttat ggtcttcaaa agggtactgt gcaactgcaa caagaaagaa 240
aaacttacca aaatctcaaa aggaaactac agcaagcttg actagacgtg tcatctttgg 300
acaagcacac acaaaaatta acattctaaa taaaaactgt cttatatgta tatacatata 360
gctttgcttt cactgttatt cagcagcata ctatacactn ttncacatca cagacatttc 420
tctattaata cataagcaca tatcttagac tatttcacag tgcttctgaa acaagtcgca 480
cagactctat tttacactat ttttctgaaa tttaagagtg cactggcaca aagaataacc 540
ttgtgaaaac ccattagtca cagactacct gctgagagaa agcagggcaa acctcactca 600
ctgatcagag acagggattt tgcagcaaga attctgagtg gctgg 645

<210> 173
<211> 516
<212> DNA
<213> Quail

<220>
<221> misc_feature
<222> (1)...(516)
<223> n = A,T,C or G

<400> 173
ccttacttcn nnnnnnnnnn nnnnnnnnnn nnnnnccttt aaaaacttgc ntcgatgcaa 60
caaatatgca catatcatta caccagttcg tccctttcca gctttacaat ggatgctgc 120
aacatgattg tcatcttcac ttagccattg gtcaagatct tcacaaaaag gtttgataag 180
ctctagctgt ggtgggttat ggtcttcaaa agggtactgt gcaactgcaa tgagaaggaa 240
taacgttcta aataaaacac agtcttgcat acagatttgc atccacacag ctttgattct 300
gttgttattc agcagcatat tacacactat aaatgcatca catgtttctc tagtaatacg 360
taagcatctt gctgcatgaa gagacctcag aagcattgtg ggaatagtta gtgctaccaa 420
ctgcacctta caccatgatt ttactcaaat taagagtgta ctggcacaaa aaataacgtg 480
ttttaaggtc acccatcaaa tgcagtgtct tttttt 516

<210> 174
<211> 395
<212> DNA
<213> Trout

<220>
<221> misc_feature
<222> (1)...(395)
<223> n = A,T,C or G

<400> 174

tctctggtcc ttacttcnnn nnnnnnnnnn nnnnnnnnnn ngctttgagg aacttgcccc 60
ggtgtaacag gtaagcacag atcatgacac ccgtacgtcc ctttccagct ttacagtgaa 120
tcgccgccac atgattgtcg tcttcactta accaaaggtc aagatcttcg cagaacggtt 180
tgatcagctc cagctggggc ggattgtgat cctcaaacgg atattgtgca actggagana 240
gacagacaga gaccgggctc agttagttag cgtcacacgt gggtttttag tgaaagattg 300
attcattcac tgactgcctg aaagacagtg ataatggttt cactctgatg taatatctaa 360
cctctgcaat tgaatttgtg ttgcgtcata atgtc 395

<210> 175
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENse sense

<400> 175
atcttgacca atggctaagt g 21

<210> 176
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Zoo44aRV

<400> 176
ttgtctctgg tccttacttc 20

<210> 177
<211> 160
<212> DNA
<213> Goat

<400> 177
tctctggtcc ttacttcccc atagaaatct agggcctctt gtgcctttaa aaatttgccc 60
cgatgtaaca aatatgcaca aatcattaca ccagttcgtc cctttccagc tttacagtga 120
attgctgcaa catgattgtc atcttcactt agccattggt 160

<210> 178
<211> 150
<212> DNA
<213> Antelope

<220>
<221> misc_feature
<222> (1)...(150)
<223> n = A,T,C or G

<400> 178
ctggtcctta cttccccata gaaatctagg gcctnntgtg cctttaaaaa tttgccccga 60
tgtaacaaat atgcacaaat cattacacca gttcgtccct ttccagcttt acagtgaatt 120
gctgcaacat gattgtcatc ttcacttagc 150

<210> 179
<211> 153

<212> DNA
<213> Kangaroo

<400> 179
tctctggtcc ttacttcccc atagaaatct agagcctctt gtgcctttaa aaactttcct 60
cgatgtaata aatatgcaca aatcattacg ccagttcgtc cctttcctgc tttacagtga 120
attgctgcaa catgattgtc atcttcactt agc 153

<210> 180
<211> 154
<212> DNA
<213> Rabbit

<400> 180
gtctctggtc cttacttctc cataaaaatc tagggcttct tgtgccttta aaaatttgcc 60
ccgatgtaat aaatatgcac aaatcattac accagttcgt ccctttccag ctttacagtg 120
aattgctgca acatgattgt catcttcact tagc 154

<210> 181
<211> 155
<212> DNA
<213> Hare

<400> 181
ggtccttact tctccataaa aatctagggc ttcttgtgcc tttaaaaatt tgccccgatg 60
taataaatat gcacaaatca ttacaccagt tcgtcccttt ccagctttac agtgaattgc 120
tgcaacatga ttgtcatctt cacttagcca ttggt 155

<210> 182
<211> 159
<212> DNA
<213> Goose

<400> 182
tctctggtcc ttacttcccc atagaaatct agagcttctt gagcctttaa aaacttgcct 60
cgatgcaaca aatatgcgca tatcattaca ccagttcgtc cctttccagc tttacagtgg 120
attgctgcaa catgattgtc atcttcactt agccattgg 159

<210> 183
<211> 156
<212> DNA
<213> Ostrich

<400> 183
ctctggtcct tacttcccca tagaaatcta gggcttcctg agcccttaaa aacttgcctc 60
gatgtaacaa ataagcacat atcattacac cagttcgtcc ctttccagct ttacagtgga 120
ttgctgcaac gtgattgtca tcttcactta gccatt 156

<210> 184
<211> 151
<212> DNA
<213> Pigeon

<400> 184
tctggtcctt acttctccgt agaaatctag ggcttcttga gcctttaaaa acttgcctcg 60
atgcaacaaa tatgcacata tcattacacc agttcgtccc tttccagctt tacagtggat 120
tgctgcaacg tgattgtcgt cttcacttag c 151

<210> 185
<211> 163
<212> DNA
<213> Varan

<400> 185
tctctggtcc ttacttcccc atagaaatct agagcttctt gtgccttttg aaatcttcct 60
cgatgtaata aatatgcaca aatcattaca ccagttcgtc cctttccagc tttacaatgg 120
attgccgcaa cgtgattgcc atcttcactt agccattggt caa 163

<210> 186
<211> 160
<212> DNA
<213> Trout

<400> 186
tctggtcctt acttcaccgt agaagtccag agcttcctgt gctttgagga acttgccccg 60
gtgtaacagg taagcacaga tcatgacacc cgtacgtccc tttccagctt tacagtgaat 120
cgccgccacg tgattgtcgt cctcacttag ccattggtca 160

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENex6F sense

<400> 187
ggagtaacta ttcccagtca gag 23

<210> 188
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENex6R antisense

<400> 188
gcaagttccg ccactgaa 18

<210> 189
<211> 138
<212> DNA
<213> Man

<400> 189
ggagtaacta ttcccagtca gaggcgctat gtgtattayt atagctacct gktaaagaat 60
catctggatt atagaccagt ggcactgttg tttcacaaga tgatgtttga aactattcca 120
atgttcagtg gcggaact 138

<210> 190
<211> 131
<212> DNA
<213> Chimpanzee

<400> 190
ctattcccag tcagaggcgc tatgtgtatt attatagcta cctgttaaag aatcatctgg 60
attatagacc agtggcactg ttgtttcaca agatgatgtt tgaaactatt ccaatgttca 120
gtggcggaac t 131

<210> 191
<211> 128
<212> DNA
<213> Cattle

<400> 191
ttcccagtca gaggcgctat gtgtattatt atagctacct gttaaagaat catctggatt 60
atagaccagt ggcactgttg tttcacaaga tgatgtttga aactattcca atgttcagtg 120
gcggaact 128

<210> 192
<211> 128
<212> DNA
<213> Sheep

<400> 192
ttcccagtca gaggcgctat gtgtattatt atagctacct gttaaagaat catctggatt 60
acagaccagt ggcactgttg tttcacaaga tgatgtttga aactattccc atgttcagtg 120
gcggaact 128

<210> 193
<211> 126
<212> DNA
<213> Goat

<400> 193
tcccagtcag aggcgctatg tgtattatta tagctacctg ttaaagaatc atctggatta 60
cagaccagtg gcactgttgt ttcacaagat gatgtttgaa actattccaa tgttcagtgg 120
cggaac 126

<210> 194
<211> 131
<212> DNA
<213> Red buffalo

<400> 194
gtaactattc ccagtcagag gcgctatgtg tattattata gctacctgtt aaagaatcat 60
ctggattata gaccagtggc actgttgttt cacaagatga tgtttgaaac tattccaatg 120
ttcagtggcg g 131

<210> 195
<211> 127
<212> DNA
<213> Deer

<400> 195
ttcccagtca gaggcgctat gtgtattatt atagctacct gttaaagaat catctggatt 60
atagaccagt ggcactgttg tttcacaaga tgatgtttga aactattcca atgttcagtg 120
gcggaac 127

<210> 196
<211> 131

<212> DNA
<213> Roe deer

<400> 196
ctattcccag tcagaggcgc tatgtgtatt attatagcta cctgttaaag aatcatctgg 60
attatagacc agtggcactg ttgtttcaca agatgatgtt tgaaactatt ccaatgttca 120
gtggcggaac t 131

<210> 197
<211> 126
<212> DNA
<213> Goitred gazelle

<400> 197
cccagtcaga ggcgctatgt gtattattat agctacctgt taaagaatca tctggattat 60
agaccagtgg cactgttgtt tcacaagatg atgtttgaaa ctattccaat gttcagtggc 120
ggaact 126

<210> 198
<211> 132
<212> DNA
<213> Horse

<400> 198
actattccca gtcagaggcg ctatgtgtat tattatagct acctgttaaa gaatcatctg 60
gattatagac cagtggcact gttgtttcac aagatgatgt ttgaaactat tccaatgttc 120
agtggcggaa ct 132

<210> 199
<211> 125
<212> DNA
<213> Dog

<400> 199
tcccagtcag aggcgctatg tgtattatta tagctacctg ttaaagaatc atctggatta 60
tagaccagtg gcactgttgt ttcacaagat gatgtttgaa actattccaa tgttcagtgg 120
cggaa 125

<210> 200
<211> 129
<212> DNA
<213> Sun bear

<400> 200
ctattcccag tcagaggcgc tatgtgtatt attatagcta cctgttaaag aatcatctgg 60
attatagacc agtggcactg ttgtttcaca agatgatgtt tgaaactatt ccaatgttca 120
gtggcggaa 129

<210> 201
<211> 128
<212> DNA
<213> Rabbit

<400> 201
ctattcccag tcagagacgc tatgtgtatt attatagcta cctgttaaag aatcatctgg 60
attatagacc agtggcactg ttgtttcaca agatgatgtt tgaaactatt ccaatgttca 120
gtggcgga 128

<210> 202
<211> 128
<212> DNA
<213> Hare

<400> 202
tattcccagt cagagacgct atgtgtatta ttatagctac ctgttaaaga atcatctgga 60
ttatagacca gtggcactgt tgtttcacaa gatgatgttt gaaactattc caatgttcag 120
tggcggaa 128

<210> 203
<211> 127
<212> DNA
<213> Antelope

<400> 203
attcccagtc agaggcgcta tgtgtattat tatagctacc tgttaaagaa tcatctggat 60
tatagaccag tggcactgtt gtttcacaag atgatgtttg aaactattcc aatgttcagt 120
ggcggaa 127

<210> 204
<211> 127
<212> DNA
<213> Kangaroo

<400> 204
tcccagtcag aggcgctatg tgtattacta tagccacctg ttaaagcatc atttggatta 60
cagaccagtg gccctgctgt ttcacaagat gatgtttgaa acaattccaa tgttcagtgg 120
cggaact 127

<210> 205
<211> 133
<212> DNA
<213> Python

<400> 205
actattccca gtcagagacg ctatgtatat tattatagct acctgttaaa gaatcatctg 60
gattacagac cagtagcact gctgtttcat aaaatgatgt ttgaaacaat tccaatgttc 120
agtggcggaa ctt 133

<210> 206
<211> 132
<212> DNA
<213> Varan

<400> 206
actattccca gtcagaggcg ctatgtatat tattacagct accttttaaa gaatcatctg 60
gattacagac ccgtggcatt gctcttccat aaaatgatgt ttgaaacaat tccaatgttc 120
agtggcggaa ct 132

<210> 207
<211> 132
<212> DNA
<213> Turkey

<400> 207
actattccca gtcagagacg ctacgtgtac tactatagct acctgttaaa gaatcacctt 60

gattacagac cagtggcact gctgtttcac aagatgatgt ttgaaacaat tcccatgttc 120
agtggcggaa ct 132

<210> 208
<211> 124
<212> DNA
<213> Chicken

<400> 208
tcccagtcag agacgctacg tgtactacta tagctacctg ttaaagaatc accttgatta 60
cagaccagtg gcactgctgt ttcacaagat gatgtttgaa acaattccca tgttcagtgg 120
cgga 124

<210> 209
<211> 127
<212> DNA
<213> Duck

<400> 209
tcccagtcag agacgctacg tgtactatta tagctacctg ttaaagaatc acctggatta 60
cagaccagtg gcactgctgt ttcacaagat gatgtttgaa acaattccca tgttcagtgg 120
cggaact 127

<210> 210
<211> 131
<212> DNA
<213> Quail

<400> 210
ctattcccag tcagagacgc tacgtgtact actatagcta cctgttaaag aatcaccttg 60
attacagacc agtggcactg ctgtttcaca agatgatgtt tgaaacaatt cccatgttca 120
gtggcggaac t 131

<210> 211
<211> 130
<212> DNA
<213> Goose

<400> 211
tattcccagt cagagacgct acgtgtacta ttatagctac ctgttaaaga atcacctgga 60
ttacagacca gtggcactgc tgtttcacaa gatgatgttt gaaacaattc ccatgttcag 120
tggcggaact 130

<210> 212
<211> 128
<212> DNA
<213> Ostrich

<400> 212
attcccagtc agagacgcta cgtgtattac tatagctacc tgttaaagaa ccacctggat 60
tacagaccag tggcactgct gtttcacaag atgatgtttg aaacaattcc aatgttcagt 120
ggcggaac 128

<210> 213
<211> 126
<212> DNA
<213> Pigeon

09936738.092701

<400> 213
cccagtcaga ggcgctacgt gtattactat agctatctgt taaagaacca cctggattac 60
agaccagtgg cactgctgtt tcacaagatg atgtttgaaa caattcccat gttcagtggc 120
ggaact 126

<210> 214
<211> 130
<212> DNA
<213> Trout

<220>
<221> misc_feature
<222> (1)...(130)
<223> n = A,T,C or G

<400> 214
attcccagtc agaggcgcta tgtctattac tatagccacc ttctcaagaa ccagctgaat 60
tacaaaccng tggctctgct cttccacaag atggtgttcg agacggtgcc catgttcagt 120
ggcggaactt 130

<210> 215
<211> 122
<212> DNA
<213> Carp

<400> 215
gtcagaggcg atatgtgtac tactatagct accttctgaa gaataagctg gagtacaaac 60
ctgtggcctt gctctttcac aagatggtgt ttgagacagt gcccatgttc agtggcggaa 120
ct 122

<210> 216
<211> 130
<212> DNA
<213> Salmon

<400> 216
tattcccagt cagaggcggt atgtctacta ctacagccac cttctgaaga accagctgga 60
gtacaaacca gtggctctgc tgttccacaa gatggtgttc gagacggtgc ccatgttcag 120
tggcggaact 130

<210> 217
<211> 132
<212> DNA
<213> Wels

<400> 217
actattccca gtcagaggcg atatgtgtac tactatagct accttctgaa gaataagctg 60
gagtacaaac ctgtggcctt gctctttcac aagatggtgt ttgagacagt gcccatgttc 120
agtggcggaa ct 132

<210> 218
<211> 129
<212> DNA
<213> Tench

<400> 218
attcccagtc agaggcgata tgtgtactac tatagctacc ttctgaagaa taagctggag 60

tacaaacctg tggccttgct ctttcacaag atggtgtttg agacagtgcc tatgttcagt 120
ggcggaact 129

<210> 219
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENex7F sense

<400> 219
cctcagtttg tggtctgcca 20

<210> 220
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENex7R antisense

<400> 220
ccttttttag catcttgttc tgttt 25

<210> 221
<211> 168
<212> DNA
<213> Man

<220>
<221> misc_feature
<222> (1)...(168)
<223> n = A,T,C or G

<400> 221
atcctcagtt tgtggtctgc cagctaaagg tgaagatata ttcctccaat tcaggaccca 60
cacgacggga agacaagttc atgtaytttg agttccctca gccgttacct gtntgtggtg 120
atatcaaagt agagttcttc cacaaacaga acaagatgct aaaaaagg 168

<210> 222
<211> 159
<212> DNA
<213> Chimpanzee

<400> 222
agtttgtggt ctgccagcta aaggtgaaga tatattcctc caattcagga cccacacgac 60
gggaagacaa gttcatgtac tttgagttcc ctcagccgtt acctgtgtgt ggtgatatca 120
aagtagagtt cttccacaaa cagaacaaga tgctaaaaa 159

<210> 223
<211> 161
<212> DNA
<213> Cattle

<400> 223
cagtttgtgg tctgccagct aaaggtgaag atatattcct ccaattcagg acccacacga 60

cgggaagaca agttcatgta ctttgagttc cctcagccat tgcctgtgtg tggtgacatc 120
aaagtagagt tcttccacaa acagaacaag atgctaaaaa a 161

<210> 224
<211> 160
<212> DNA
<213> Sheep

<400> 224
gtttgtggtc tgccagctaa aggtgaagat atattcctcc aattcaggac ccacacgacg 60
ggaagacaag ttcatgtact ttgagttccc tcagccgctg cctgtgtgtg gtgacatcaa 120
agtagagttc ttccacaaac agaacaagat gctaaaaaag 160

<210> 225
<211> 161
<212> DNA
<213> Goat

<400> 225
cagtttgtgg tctgccagct aaaggtgaag atatattcct ccaattcagg acccacacga 60
cgggaagaca agttcatgta ctttgagttc cctcagccgt tgcctgtgtg tggtgacatc 120
aaagtagagt tcttccacaa acagaacaag atgctaaaaa a 161

<210> 226
<211> 153
<212> DNA
<213> Red buffalo

<400> 226
agtttgtggt ctgccagcta aaggtgaaga tatattcctc caattcagga cccacacgac 60
gggaagacaa gttcatgtac tttgagttcc ctcagccgtt gcctgtgtgt ggtgacatca 120
aagtagagtt cttccacaaa cagaacaaga tgc 153

<210> 227
<211> 159
<212> DNA
<213> Deer

<400> 227
cagtttgtgg tctgccagct aaaggtgaag atatattcct ccaattcagg acccacacga 60
cgggaagaca agttcatgta ctttgagttc cctcagccgt tgcctgtgtg tggtgacatc 120
aaagtagagt tcttccacaa acagaacaag atgctaaaa 159

<210> 228
<211> 162
<212> DNA
<213> Roe deer

<400> 228
cagtttgtgg tgtgccagct aaaggtgaag atatattcct ccaattcagg acccacacga 60
cgggaagaca agttcatgta ctttgagttc cctcagccgt tgcctgtgtg tggtgacatc 120
aaagtagagt tcttccacaa acagaacaag atgctaaaaa ag 162

<210> 229
<211> 161
<212> DNA
<213> Goitred gazelle

<400> 229
cagtttgtgg tctgccagct aaaggtgaag atatattcct ccaattcagg acccacacga 60
cgggaagata agttcatgta ctttgagttc cctcagccgt tgcctgtgtg tggtgacatc 120
aaagtagagt tcttccacaa acagaacaag atgctaaaaa a 161

<210> 230
<211> 162
<212> DNA
<213> Horse

<400> 230
tcagtttgtg gtctgccagc taaaggtgaa gatatattcc tccaattcag gacccacacg 60
acgggaagac aagttcatgt actttgagtt ccctcagccg ttgcctgtgt gtggtgacat 120
caaagtagag ttcttccaca aacagaacaa gatgctaaaa aa 162

<210> 231
<211> 162
<212> DNA
<213> Dog

<400> 231
tcagtttgtg gtctgccagc taaaggtgaa gatctattcc tccaattcag gacccacacg 60
acgggaagac aagttcatgt actttgagtt ccctcagcca ttgcctgtgt gcggtgacat 120
caaagtagag ttcttccaca aacagaacaa gatgctaaaa aa 162

<210> 232
<211> 161
<212> DNA
<213> Sun bear

<400> 232
cagtttgtgg tctgccagct aaaggtgaag atctattcct ccaattcagg acccacacga 60
cgggaagaca agttcatgta cttcgagttc cctcagccgt tacctgtgtg tggtgacatc 120
aaagtagagt tcttccacaa acagaacaag atgctaaaaa a 161

<210> 233
<211> 162
<212> DNA
<213> Rabbit

<400> 233
cagtttgtgg tctgccagct aaaggtgaag atatattcct ccaattcagg acccacacga 60
cgggaagaca agttcatgta cttcgagttc cctcagccgt tgcctgtgtg tggtgacatc 120
aaagtagagt tcttccacaa acagaacaag atgctaaaaa ag 162

<210> 234
<211> 156
<212> DNA
<213> Hare

<400> 234
ctcagtttgt ggtctgccag ctaaaggtga agatatattc ctccaattca ggacccacac 60
gacgggaaga caagttcatg tacttcgagt tccctcagcc gttgcctgtg tgtggtgaca 120
tcaaagtaga gttcttccac aaacagaaca agatgc 156

<210> 235
<211> 160

<212> DNA
<213> Antelope

<220>
<221> misc_feature
<222> (1)...(160)
<223> n = A,T,C or G

<400> 235
tcagtttgtg gtctgccagc taaaggtgaa gatatattcc tccaannnag gacccacacg 60
acgggaagac aagttcatgt actttgagtt ccctcagccg ttgcctgtgt gtggtgatat 120
caaagtagag ttcttccaca aacagaacaa gatgctaaaa 160

<210> 236
<211> 163
<212> DNA
<213> Kangaroo

<400> 236
ctcagtttgt ggtctgccag ctgaaggtga agatctacac atccccgtca gggcccacgc 60
ggcgggaaga caagcacatg tacttcgagt tcccccagcc tctgccggtg tgtggcgaca 120
ttaaagtgga attcttccac aaacagaaca agatgctaaa aaa 163

<210> 237
<211> 145
<212> DNA
<213> Turkey

<220>
<221> misc_feature
<222> (1)...(145)
<223> n = A,T,C or G

<400> 237
cagtttgtgg tctgccagct aaaagtaaag atattcacct ccccttnnng accctcaaga 60
cgtgaagaca aatatatgta cttngaattc cctcaacctt tgccggnata cggtgatatc 120
aaagnggagt tcttccacaa acaga 145

<210> 238
<211> 146
<212> DNA
<213> Chicken

<400> 238
cagtttgtgg tctgccagct aaaggtaaag atattcacct ccccttcagg accctcaaga 60
cgtgaagaca agtatatgta ctttgaattc cctcaacctt tgccggtatg cggtgatatc 120
aaagtggagt tcttccacaa acagaa 146

<210> 239
<211> 154
<212> DNA
<213> Duck

<400> 239
cagtttgtgg tctgccagct aaaggtaaag atattcacct ccccttcagg accctcaaga 60
cgtgaagaca agtatatgta ctttgaattc cctcaacctt tgccggtatg cggtgatatc 120
aaagtggtgt tttccacaa acagaacaag atgc 154

<210> 240
<211> 163
<212> DNA
<213> Quail

<400> 240
tcagtttgtg gtctgccagc taaaggtaaa gatattcacc tccccttcag gaccctcaag 60
acgtgaagac aagtatatgt actttgaatt ccctcaacct ttgccggtat gcggtgatat 120
caaagtggag ttcttccaca aacagaacaa gatgctaaaa aag 163

<210> 241
<211> 160
<212> DNA
<213> Ostrich

<400> 241
gtttgtggtc tgccagctaa aggtaaagat attcacctcc ccttcaggac cctcaagacg 60
tgaagacaag tatatgtact ttgaattccc tcaacccttg ccggtatgcg gtgatatcaa 120
agtggaattc ttccacaaac agaacaagat gctaaaaaag 160

<210> 242
<211> 145
<212> DNA
<213> Pigeon

<400> 242
tcagtttgtg gtctgccagc taaaggtaaa gatattcacc tccccttcag gaccctcaag 60
acgtgaagac aagtatatgt actttgaatt ccctcaacct ttgccggtat gcggtgatat 120
caaagtggaa tttttccaca aacag 145

<210> 243
<211> 163
<212> DNA
<213> Carp

<220>
<221> misc_feature
<222> (1)...(163)
<223> n = A,T,C or G

<400> 243
tcagtttgtg gtctgccaac tgaaggtgaa aatccacacc tcaaacccag ygcacacaag 60
gcgagaggag aagtacatgt acttngattt tccncagcnn ctgcctgtgt gnggagacat 120
caaggtggag ttcttccaca aacagaacaa gatgctaaaa aag 163

<210> 244
<211> 160
<212> DNA
<213> Wels

<220>
<221> misc_feature
<222> (1)...(160)
<223> n = A,T,C or G

<400> 244
agtttgtggt ctgccaactg aaggtgaaaa tccacacatc aaacccagng cacacaaggc 60

gagaggagaa gtacatgtac ttngattttc cncagcnnct gcctgtgtgn ggagacatca 120
aggtggagtt cttccacaaa cagaacaaga tgctaaaaaa 160

<210> 245
<211> 159
<212> DNA
<213> Tench

<400> 245
agtttgtggt ctgccagctg aaggtgaaaa tccacacctc caacccagcg cacacaaggc 60
gagaggagaa atacatgtac ttcgagtttc cacagccatt gcctgtgtgt ggagacatca 120
aggtggagtt cttccacaaa cagaacaaga tgctaaaaa 159

<210> 246
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENex8F sense

<400> 246
caaaatgttt cacttttggg taaa 24

<210> 247
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENex8R antisense

<400> 247
taaaatttgg agaaaagtat cggtt 25

<210> 248
<211> 226
<212> DNA
<213> Man

<400> 248
gacaaaaatg tttcactttt gggtaaatac attcttcata ccaggaccag aggaaacctc 60
agaaaaagta gaaaatggaa gtctatgtga tcaagaaaty gatagcattt gcagtataga 120
gcgtgcagat aatgacaagg artatctagt acttacttta acaaaaaatg atcttgacaa 180
agcaaataaa gacaaagcca accgatactt ttctccaaat tttaag 226

<210> 249
<211> 213
<212> DNA
<213> Chimpanzee

<400> 249
atgtttcact tttgggtaaa tacattcttc ataccaggac cagaggaaac ctcagaaaaa 60
gtagaaaatg gaagtctatg tgatcaagaa atcgatagca tttgcagtat agagcgtgca 120
gataatgaca aggaatatct agtacttact ttaacaaaaa atgatcttga caaagcaaat 180
aaagacaaag ccaaccgata cttttctcca aat 213

09936738.091701

<210> 250
<211> 212
<212> DNA
<213> Cattle

<400> 250
tgtttcactt ttgggtaaac acattcttca taccaggacc agaggaaacc tcagaaaaag 60
tagaaaatgg aagtctatgt gatcaagaaa ttgatagtat ttgcagtata gagcgtgcag 120
ataatgacaa ggaatatcta gtactcactt taacaaaaaa tgatctcgac aaagcaaata 180
aagacaaggc caaccgatac ttttctccaa at 212

<210> 251
<211> 211
<212> DNA
<213> Sheep

<400> 251
gtttcacttt tgggtaaaca cattcttcat accaggacca gaggaaacct cagaaaaagt 60
agaaaatgga agtctatgtg atcaagaaat tgatagtatt tgcagtatag agcgtgcaga 120
taatgacaag gaatatctag tgctcacttt aacaaaaaat gatctcgaca aagcaaataa 180
agacaaggcc aaccgatact tttctccaaa t 211

<210> 252
<211> 213
<212> DNA
<213> Goat

<400> 252
atgtttcact tttgggtaaa cacattcttc ataccaggac cagaggaaac ctcagaaaaa 60
gtagaaaatg gaagtctatg tgatcaagaa attgatagta tttgcagtat agagcgtgca 120
gataatgaca aggaatatct agtactcact ttaacaaaaa atgatcttga caaagcaaat 180
aaagacaagg ccaaccgata cttttctcca aat 213

<210> 253
<211> 212
<212> DNA
<213> Red buffalo

<400> 253
atgtttcact tttgggtaaa cacattcttc ataccaggac cagaggaaac ctcagaaaaa 60
gtagaaaatg gaagtctatg tgatcaagaa attgatagta tttgcagtat agagcgtgca 120
gataatgaca aggaatatct agtactcact ttaacaaaaa atgatctcga caaagcaaat 180
aaagacaagg ccaaccgata cttttctcca aa 212

<210> 254
<211> 213
<212> DNA
<213> Deer

<400> 254
tgtttcactt ttgggtaaac acattcttca taccaggacc agaggaaacc tcagaaaaag 60
tagaaaatgg aagtctatgt gatcaagaaa ttgatagtat ttgcagtata gagcgtgcag 120
ataatgacaa agaatatcta gtactcactt taacaaaaaa tgatctcgac aaagcaaata 180
aagacaaggc caaccgatac ttttctccaa att 213

<210> 255
<211> 214

<212> DNA
<213> Roe deer

<400> 255
atgtttcact tttgggtaaa cacattcttc ataccaggac cagaggaaac ctcagaaaaa 60
gtagaaaatg gaagtctatg tgatcaagaa attgatagta tttgcagtat agagcgtgca 120
gataatgaca aagaatatct agtactcact ttaacaaaaa atgatctcga caaagcaaat 180
aaagacaagg ccaaccgata cttttctcca aatt 214

<210> 256
<211> 213
<212> DNA
<213> Goitred gazelle

<400> 256
atgtttcact tttgggtaaa cacattcttc ataccaggac cagaggaaac ctcagaaaaa 60
gtagaaaatg gaagtctatg tgatcaagaa attgatagta tttgcagtat agagcgtgca 120
gataatgaca aggaatatct agtactcact ttaacaaaaa atgatctcga caaagcaaat 180
aaagacaagg ccaaccgata cttttctcca aat 213

<210> 257
<211> 213
<212> DNA
<213> Horse

<400> 257
atgtttcact tttgggtaaa tacattcttt ataccaggac cagaggaaac ctcagaaaaa 60
gtagaaaatg gaagtctatg tgatcaagaa attgatagta tttgcagtat agagcgtgca 120
gataatgaca aagaatatct agtactcact ttaacaaaaa atgatctcga caaagcaaat 180
aaagacaagg ccaaccgata cttttctcca aat 213

<210> 258
<211> 210
<212> DNA
<213> Dog

<400> 258
tttcactttt gggtaaacac attcttcata ccaggaccag aggaaacctc agaaaaagta 60
gaaaatggaa gtctatgtga tcaagaaatt gatagtattt gcagtataga acgtgcagat 120
aatgacaagg aatatctagt actcacttta acaaaaaatg atctcgacaa agcaaataaa 180
gacaaggcca accgatactt ttctccaaat 210

<210> 259
<211> 213
<212> DNA
<213> Sun bear

<400> 259
atgtttcact tttgggtaaa cacattcttc ataccaggac cagaggaaac ctcagaaaaa 60
gtagaaaatg gaagtctatg tgatcaagaa attgatagta tttgcagtat agagcgtgca 120
gataatgaca aggaatatct agtactcact ttaacaaaaa atgatctcga caaagcaaat 180
aaagacaagg ccaaccgata cttttctcca aat 213

<210> 260
<211> 210
<212> DNA
<213> Rabbit

<400> 260
tttcactttt gggtaaatac gttctttata ccaggaccag aggaaacctc agaaaaagta 60
gaaaatggaa gtctttgtga tcaagaaatt gatagtattt gcagtataga acgtgcagat 120
aacgacaaag aatatctagt acttacttta acaaaaaatg atcttgataa agcaaataaa 180
gacaaggcaa accgatactt ttctccaaat 210

<210> 261
<211> 210
<212> DNA
<213> Hare

<400> 261
gtttcacttt tgggtaaata cgttctttat accaggacca gaggaaacct cagaaaaagt 60
agaaaatgga agtctttgtg atcaagaaat tgatagtatt tgcagtatag aacgtgcaga 120
taacgacaaa gaatatctag tacttacttt aacaaaaaat gatcttgata aagcaaataa 180
agacaaggca aaccgatact tttctccaaa 210

<210> 262
<211> 203
<212> DNA
<213> Antelope

<400> 262
acttttgggt aaatacattc ttcataccag gaccagagga aacctcagaa aaagtagaaa 60
atggaagtct atgtgatcaa gaaattgata gtatttgcag tatagagcgt gcagataatg 120
acaaggaata tctagtactc actttaacaa aaaatgatct tgacaaagca aataaagaca 180
aggccaaccg atacttttct cca 203

<210> 263
<211> 213
<212> DNA
<213> Kangaroo

<400> 263
tttcactttt gggtaaatac attcttcata ccaggaccag aggaaaattc agacaaagta 60
gaaaatggaa gtctttgtgg tgatcaagag attgatagta tttgcagtgc cgagcgatca 120
gataatgaca aggaatatct catactcaca ttatccaaaa atgatcttga caaagcgaat 180
aaagacaagg ccaaccgata cttttctcca aat 213

<210> 264
<211> 210
<212> DNA
<213> Python

<400> 264
tttcactttt gggtaaatac attcttcata ccaggaccag aggaaacctc agaaaaagta 60
gaaaatggaa gtctatgtga tcaagaaatc gatagcattt gcagtataga gcgtgcagat 120
aatgacaagg aatatctagt acttacttta acaaaaaatg atcttgacaa agcaaataaa 180
gacaaagcca accgatactt ttctccaaat 210

<210> 265
<211> 208
<212> DNA
<213> Turkey

<400> 265
tcacttttgg gtaaatacat tcttcatagg actggatgaa aattcagaca aagtagaaaa 60

tggaagtcta gttgcagatc aggaacttga tggtattttc agtacagagc gctcagataa 120
tgacaaggaa tatttaatcc ttacattaac aaaaaatgat ctagacaaag caaataaaga 180
caaagccaac cgatactttt ctccaaat 208

<210> 266
<211> 213
<212> DNA
<213> Chicken

<400> 266
tttcactttt gggtaaatac attcttcata ggactggatg aaaattcaga caaagtagaa 60
aatggaagtc tagttgcaga tcaggaactt gatggtattt tcagtacaga gcgctcagat 120
aatgacaagg aatatttaat ccttacatta acaaaaaatg atctagacaa agcaaataaa 180
gacaaagcca accgatactt ttctccaaat tta 213

<210> 267
<211> 210
<212> DNA
<213> Quail

<400> 267
ttcacttttg ggtaaataca ttcttcatag gactggatga aaattcagac aaagtagaaa 60
atggaagtct agttgcagat caggaacttg atggtatttt cagtacagag cgctcagata 120
atgacaagga atatttaatc cttacattaa caaaaaacga tctagacaaa gcaaataaag 180
acaaagccaa ccgatacttt tctccaaatt 210

<210> 268
<211> 213
<212> DNA
<213> Goose

<400> 268
atgtttcact tttgggtaaa tacattcttc ataggactgg atgaaaattc agacaaagta 60
gaaaatggaa gtctagttgc agatcaggaa cttgatggta ttttcagtac agagcgctca 120
gataatgata aggaatattt aatccttaca ttaacaaaaa atgatctaga caaagcaaat 180
aaagacaaag ccaaccgata cttttctcca aat 213

<210> 269
<211> 235
<212> DNA
<213> Trout

<220>
<221> misc_feature
<222> (1)...(235)
<223> n = A,T,C or G

<400> 269
gtttcacttt tgggtaaatn nnttctttgt ccctggacca gaggagaact ttgagaaggt 60
tgagaacggg acgttaccaa cggagacgtt accaacggcg acgttaccaa aggagcaggc 120
aggaaaccaa acgggaggaa cgggggacaa cgacaaggat tacctgatcc tctcactgac 180
aaagaacgac ctggacaagg ccaacaagga taaabcaaac cgatactttt ctcca 235

<210> 270
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENex9F sense

<400> 270
gtgaagctgt acttcacaaa aac 23

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PTENex9tga antisense

<400> 271
aaaaaaattc agacttttgt aatttg 26

<210> 272
<211> 194
<212> DNA
<213> Man

<400> 272
gtgaagctgt acttcacaaa aacagtagag gagccgtcaa atccagaggc tagcagttca 60
acttctgtaa caccagatgt tagtgacaat gaacctgatc attatagata ttctgacacc 120
actgactctg atccagagaa tgaacctttt gatgaagatc agcatacaca aattacaaaa 180
gtctgaattt tttt 194

<210> 273
<211> 180
<212> DNA
<213> Chimpanzee

<400> 273
gtacttcaca aaaacagtag aggagccgtc aaatccagag gctagcagtt caacttctgt 60
aacaccagat gttagtgaca atgaacctga tcattataga tattctgaca ccactgactc 120
tgatccagag aatgaacctt ttgatgaaga tcagcataca caaattacaa aagtctgaat 180

<210> 274
<211> 176
<212> DNA
<213> Cattle

<400> 274
cttcacaaaa acagtagagg agtcatcaaa tccagaggct agcagttcaa cttctgtaac 60
accagatgtt agtgacaatg aacctgatca ttatagatat tctgacacca ctgactctga 120
tccagagaat gaacctttg atgaagatca gcatacacaa attacaaaag tctgaa 176

<210> 275
<211> 172
<212> DNA
<213> Sheep

<400> 275
cttcacaaaa acagtagagg agtcatcaaa tccagaggct agcagttcaa cgtctgtaac 60
accagatgtc agtgacaatg aacctgatca ttacagatat tctgacacca ctgactctga 120

cccagagaat gaacctttg atgaagatca gcatacacaa attacaaaag tc 172

<210> 276
<211> 178
<212> DNA
<213> Goat

<400> 276
tacttcacaa aaacagtaga ggagtcatca aatccagagg ctagcagttc aacgtctgta 60
acaccagatg tcagtgacaa tgaacctgat cattacagat attctgacac cactgactct 120
gacccagaga atgaaccttt tgatgaagat cagcatacac aaattacaaa agtctgaa 178

<210> 277
<211> 179
<212> DNA
<213> Red buffalo

<400> 277
tacttcacaa aaacagtaga ggagccatca aatccagagg ctagcagttc cacttctgtg 60
acacccgatg ttagtgacaa tgaacctgat cattatagat attctgacac cactgactct 120
gatccagaga atgaaccttt tgatgaagat cagcatacac aaattacaaa agtctgaat 179

<210> 278
<211> 179
<212> DNA
<213> Deer

<400> 278
tacttcacaa aaacagtaga ggagtcatca aatccagagg ctagcagttc aacttctgta 60
acaccagatg ttagtgacaa tgaacctgat cattatagat attctgacac cactgactct 120
gatccagaga atgaaccttt tgatgaagat cagcatacac aaattacaaa agtctgaat 179

<210> 279
<211> 173
<212> DNA
<213> Roe deer

<400> 279
acttcacaaa aacagtagag gagtcatcaa atccagaggc tagcagttca acttctgtaa 60
caccagatgt tagtgacaat gaacctgatc attatagata ttctgacacc actgactctg 120
atccagagaa tgaacctttt gatgaagatc agcatacaca aattacaaaa gtc 173

<210> 280
<211> 177
<212> DNA
<213> Goitred gazelle

<400> 280
cttcacaaaa acagtagagg agtcatcaaa tccagaggct agcagttcaa cgtctgtaac 60
accagatgtc agtgacaatg aacctgatca ttacagatat tctgacacca ctgactctga 120
cccagagaat gaacctttg atgaagatca gcatacacaa attacaaaag tctgaat 177

<210> 281
<211> 180
<212> DNA
<213> Horse

<400> 281
gtacttcaca aaaacagtag aggagccatc aaatccagag gctagcagtt caacttctgt 60
aacaccagat gttagtgaca atgaacctga tcattataga tattctgaca ccactgactc 120
tgatccagag aatgaacctt ttgatgaaga tcagcataca caaattacaa aagtctgaat 180

<210> 282
<211> 180
<212> DNA
<213> Dog

<400> 282
gtacttcaca aaaactgtag aggagccatc aaacccggag gctagcagtt caacttctgt 60
gacgccagat gttagtgaca atgaacctga tcattataga tattctgaca ccactgactc 120
tgacccagag aatgaaccct ttgatgaaga tcagcacaca caaattacaa aagtctgaat 180

<210> 283
<211> 177
<212> DNA
<213> Sun bear

<400> 283
cttcacaaaa acagtagagg agccatcaaa tcccgaggct agcagttcaa cttctgtaac 60
accagacgtt agtgacaatg aacctgacca ttatcgatat tctgacacca ctgactctga 120
tccagagaat gaacctttg atgaagatca gcatacacaa attacaaaag tctgaat 177

<210> 284
<211> 177
<212> DNA
<213> Rabbit

<400> 284
tacttcacaa aaacagtaga ggagccatca aatccagagg ctagcagttc aacttctgta 60
acgccagatg ttagtgacaa tgaacctgat cattatagat attctgacac cactgactct 120
gatccagaga atgaaccttt tgatgaagat cagcatacac aaattacaaa agtctga 177

<210> 285
<211> 179
<212> DNA
<213> Hare

<220>
<221> misc_feature
<222> (1)...(179)
<223> n = A,T,C or G

<400> 285
tacttcacaa aaacagtaga ggagccatca aatccagagg ctagcagttc aacttctgta 60
acgccagatg ttagtgacaa tgancctgat cattatagat attctgacac cactgactct 120
gatccagaga atgaaccttt tgatgaagat cagcatacac aaattacaaa agtctgaat 179

<210> 286
<211> 175
<212> DNA
<213> Antelope

<400> 286
acttcacaaa aacagtagag gagccatcaa atccagaggc tagcagttca acttctgtaa 60
caccagatgt tagtgacaat gaacctgatc attatagata ytctgacacc actgactctg 120
atccagagaa tgaacctttt gatgaagatc agcatacaca aattacaaaa gtctg 175

<210> 287
<211> 174
<212> DNA
<213> Varan

<400> 287
ttcacaaaaa ccgtagaaga accatcaaac ccagaggcta gcagctcaac ttcagtaacg 60
ccagatgtta gtgataatga acctgatcat tataggtatt ctgataccac tgactctgat 120
ccagagaatg aaccttttga tgaagatcag catacacaaa ttacaaaagt ctga 174

<210> 288
<211> 175
<212> DNA
<213> Turkey

<400> 288
ttcacaaaaa cagtagagga gccatcaaat ccagaggcta gcagttcaac ttctgtaaca 60
ccagatgtta gtgacaatga acctgatcat tatagatatt ctgacaccac tgactctgat 120
ccagagaatg aaccttttga tgaagatcag catacacaaa ttacaaaagt ctgaa 175

<210> 289
<211> 182
<212> DNA
<213> Chicken

<400> 289
ctgtacttca caaaaacagt agaagagcca tcaaatcccg aggctagcag ttcaacttct 60
gtaacaccag atgttagtga caatgaacct gatcattaca gatactctga caccactgac 120
tctgatccag agaatgaacc ttttgatgaa gatcagcata cacaaattac aaaagtctga 180
at 182

<210> 290
<211> 177
<212> DNA
<213> Duck

<400> 290
cttcacaaaa acagtagaag agccatctaa tccagaggct agcagttcaa cttctgtaac 60
gccagatgtt agtgacaatg aacctgatca ttatagatac tctgacacca ctgactctga 120
tccagagaat gaaccttttg atgaagatca gcatacgcaa attacaaaag tctgaat 177